



IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re Patent Application of:  
Timothy A. Coleman

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Group Art Unit: 1653

Filed: August 3, 2001

Examiner: Not Yet Assigned

For: Vascular Endothelial Growth Factor 2

**SUBMISSION OF REPLACEMENT/SUBSTITUTE DRAWINGS**

Attn: Draftsperson  
Commissioner for Patents  
Washington, DC 20231

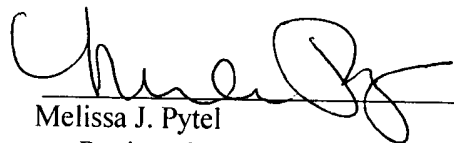
Sir:

Applicants submit herewith replacement/substitute Figures 1A-31U (68 sheets) to replace Figures 1A-31G (47 sheets) as originally filed. Additional pages are due to reorganization of the drawings in order to comply with the margin requirements under 37 C.F.R. § 1.84. No new matter is introduced.

No fee is believed due for this submission. In the event that a fee is required in connection with this submission, please charge the required fee to Deposit Account No. 08-3425.

Respectfully submitted,

Dated: April 17, 2003

  
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1	60	GTCCTTCCACCATGCACTCGCTGGGCTTCTTCTCTGTGGCGTGTCTCTCTGCTCGCCGCTG -----+-----+-----+-----+-----+-----+-----+-----+ CAGGAAGGTGGTACGTGAGCGACCCGAAGAAGAGACACCGCACAAAGACGAGCGGGGAC M H S L G F F S V A C S L L A A A
61	120	CGCTGCTCCCGGCTCTCGGAGGCGCCCGCCGCGCCGCGCCCTTCGAGTCCGGACTCG -----+-----+-----+-----+-----+-----+-----+-----+ GCGACGAGGGCCAGGAGCGCTCCGGGGCGGGCGGGCGGGAAGCTCAGGCCCTGAGC L L P G P R E A P A A A A A F E S G L D
121	180	ACCTCTCGGACGGGAGCCCGACGCGGGCGAGGCCACGGCTTATGCAAGCAAGATCTGG -----+-----+-----+-----+-----+-----+-----+-----+ TGGAGAGCCTGCGCCTCGGGCTGCGCCCGCTCCGGTGCCGAATACGTTCTGTTCTAGACC L S D A E P D A G E A T A Y A S K D L E
181	240	AGGAGCAGTTACGGTCTGTGCCAGTGTAGATGAACTCATGACTGTACTCTACCCAGAAT -----+-----+-----+-----+-----+-----+-----+-----+ TCCTCGTCAATGCCAGACACAGGTCACATCTACTTGAGTACTGACATGAGATGGGTCTTA E Q L R S V S S V D E L M T V L Y P E Y
241	300	ATTGGAAAATGTACAAGTGTGTCAGCTAAGGAAAGGAGGCTGGCAACATAACAGAGAACAGG -----+-----+-----+-----+-----+-----+-----+-----+ TAACCTTTTACATGTTACAGTCGATTCCCTTTCCTCCGACCGTTGTATTGTCTCTTGTCC W K M Y K C Q L R K G G W Q H N R E Q A
301	360	CCAACCTCAACTCAGGACAGAAAGAGACTATAAAATTTGCTGCAGCACATTATAATACAG -----+-----+-----+-----+-----+-----+-----+-----+ GGTTGGAGTTGAGTTCCTGTCTTCTCTGATATTTAAACGACGTCGTGTAATATATGTC N L N S R T E E T I K F A A A H Y N T E

FIG. 1A

MATCH WITH FIG. 1B

MATCH WITH FIG. 1A

361 AGATCTTGAAAAAGTATTGATAATGAGTGGAGAAAAGACTCAATGCATGCCACGGGAGGTGT  
-----+-----+-----+-----+-----+-----+-----+-----+  
TCTAGAACTTTTCATAAATACTACTCACCTCTTTCTGAGTTACGTACGGTGCCCTCCACA  
I L K S I D N E W R K T Q C M P R E V C  
420  
GTATAGATGTGGGAAGGAGTTTGGAGTCGCGACAAACACCTTCTTTAAACCTCCATGTG  
-----+-----+-----+-----+-----+-----+-----+-----+  
CATATCTACACCCCTTCCCTCAAAACCTCAGCGCTGTTGTGGAAGAAATTTGGAGGTACAC  
I D V G K E F G V A T N T F F K P P C V  
480  
TGTCCTCTACAGATGTGGGGGTGCTGCAATAGTGAGGGGCTGCAGTGCATGAACACCA  
-----+-----+-----+-----+-----+-----+-----+-----+  
ACAGGCAGATGTCTACACCCCCCAACGACGTTATCACTCCCCGACGTCACGTACTTGTGGT  
S V Y R C G G C C N S E G L Q C M N T S  
540  
GCACGAGCTACCTCAGCAAGACGTTATTTGAAATTACAGTGCCTCTCTCTCAAGGCCCCCA  
-----+-----+-----+-----+-----+-----+-----+-----+  
CGTGCTCGATGGAGTCGTTCTGCAATAAACTTTAATGTCACGGAGAGAGAGTTCCGGGGT  
T S Y L S K T L F E I T V P L S Q G P K  
600  
AACCAGTAACAATCAGTTTGGCCAATCACACTTCCTGCCGATGCATGTCTAAACTGGATG  
-----+-----+-----+-----+-----+-----+-----+-----+  
TTGGTCAATTGTAGTCAAAACGGTTAGTGTGAAGGACGGCTACGTACAGATTTGACCTAC  
P V T I S F A N H T S C R C M S K L D V  
660

MATCH WITH FIG. 1C

FIG. 1B

**FIG. 1C**

**MATCH WITH FIG. 1D**

661		TTTACAGACAAGTTCATTCCATTTATTAGACGTTCCCTGCCAGCAACTACCACAGTGTC -----+-----+-----+-----+-----+-----+ AAATGTCTGTTCAAGTAAGGTAATAA TCTGCAAGGACGGTCGTTGTGATGGTGTCA CAG Y R Q V H S I I R R S L P A T L P Q C Q	720
721		AGGCAGCGAACAAGACCTGCCCCCCACCAATTACATGTGGAATAATCACATCTGCAGATGCC -----+-----+-----+-----+-----+-----+ TCCGTCGCTTGTCTGGACGGGGTGGTTAATGTAACACCTTATTAGTGTAGACGCTACGG A A N K T C P T N Y M W N N H I C R C L	780
781		TGGCTCAGGAAGATTTTATGTTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCC -----+-----+-----+-----+-----+-----+ ACCGAGTCCTTCTAAAAATACAAAAGGAGCCTACGACCTCTACTGAGTTGTCTACCTAAGG A Q E D F M F S S D A G D D S T D G F H	840
841		ATGACATCTGTGGACCAAACAAGGAGCTGGATGAAGAGACCTGTCTAGTGTCTGTCAGAG -----+-----+-----+-----+-----+-----+ TACTGTAGACACCTGGTTTGTTCCTCGACCTACTTCTCTGGACAGTCACACAGACGTCTC D I C G P N K E L D E E T C Q C V C R A	900
901		CGGGGCTTCGGCCTGCCAGCTGTGGACCCCACAAAGAACTAGACAGAAACTCATGCCAGT -----+-----+-----+-----+-----+-----+ GCCCCGAAGCCGACGGTCGACACCTGGGGTGTTCCTTGATCTGTCTTTGAGTAGCGTCA G L R P A S C G P H K E L D R N S C Q C	960

MATCH WITH FIG. 1C

961 GTGCTGTGTAACAACTCTTCCCCAGCCCAATGTGGGGCCAAACCGAGAAATTTGATGAAA  
-----+-----+-----+-----+-----+-----+-----+  
CACAGACATTTTGTGAGAAAGGGTCCGGTTACACCCCGGTGGCTCTTAAACTACTTT  
V C K N K L F P S Q C G A N R E F D E N  
1020

1021 ACACATGCCAGTGTGTATGTAAAGAACCTGCCCCAGAAATCAACCCCTAAATCCTGGAA  
-----+-----+-----+-----+-----+-----+-----+  
TGTGTACGGTCACACATACATTTCTTGGACGGGTCTTTAGTTGGGATTTAGGACCTT  
T C Q C V C K R T C P R N Q P L N P G K  
1080

1081 AATGTGCCCTGTGAATGTACAGAAAGTCCACAGAAATGCTTGTAAAAGGAAAGAGTTCC  
-----+-----+-----+-----+-----+-----+-----+  
TTACACGGACACTTACATGTCTTTCAGGTGTCTTTACGAACAATTTTCCCTTCTCAAGG  
C A C E C T E S P Q K C L L K G K K F H  
1140

1141 ACCACCAACATGCAGCTGTTACAGACGGCCCATGTACGAACCCGACAGAGGCTGTGAGC  
-----+-----+-----+-----+-----+-----+-----+  
TGCTGGTTGTACGTCGACAATGTCTGCCGGTACATGCTTGGCGGTCTTCCGAAACACTCG  
H Q T C S C Y R R P C T N R Q K A C E P  
1200

1201 CAGGATTTTCATATAGTGAAGAAGTGTGTGCTTGTGTCCCTTCATATTTGGCAAAGACCAC  
-----+-----+-----+-----+-----+-----+-----+  
GTCCTAAAAGTATACACTTCTTACACAGCAACACAGGGAAGTATAACCGTTTCTGGTG  
G F S Y S E E V C R C V P S Y W Q R P Q  
1260

FIG. 1D

MATCH WITH FIG. 1E

**MATCH WITH FIG. 1D**

[illegible]

**FIG. 1E**

```

1      . . . . .
      CGAGGCCACGGCTTATGCAAGCAAAAGATCTGGAGGAGCAGTTACGGTCTGTGTCCAGTGT
      -----+-----+-----+-----+-----+-----+-----+
61     . . . . .
      AGATGAACTCATGACTGTACTCTACCCAGAATAATTGGAATAATGTACAAGTGTCAAGCTAAG
      -----+-----+-----+-----+-----+-----+-----+
           M T V L Y P E Y W K M Y K C Q L R
           -----+-----+-----+-----+-----+-----+
121    . . . . .
      GAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAAGAGAC
      -----+-----+-----+-----+-----+-----+-----+
           K G G W Q H N R E Q A N L N S R T E E T
           -----+-----+-----+-----+-----+-----+
181    . . . . .
      TATAAAATTTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAATGAGTG
      -----+-----+-----+-----+-----+-----+-----+
           I K F A A A H Y N T E I L K S I D N E W
           -----+-----+-----+-----+-----+-----+
241    . . . . .
      GAGAAAGACTCAATGCATGCCACGGGAGGTGTGTATAGATGTGGGGAAGGAGTTTGAGT
      -----+-----+-----+-----+-----+-----+-----+
           R K T Q C M P R E V C I D V G K E F G V
           -----+-----+-----+-----+-----+-----+
301    . . . . .
      CGCGACAAACACCTTCTTTAAACCTCCATGTGTGTCCGTCTACAGATGTGGGGGTTGCTG
      -----+-----+-----+-----+-----+-----+-----+
           A T N T F F K P P C V S V Y R C G G C C
  
```

FIG. 2A

MATCH WITH FIG. 2B

MATCH WITH FIG. 2A

421 TGAAATTACAGTGCCTCTCTCTCAAGGCCCCCAACCAGTAACAATCAGTTTGGCCAATCA  
-----+-----+-----+-----+-----+  
E I T V P L S Q G P K P V T I S F A N H

481 CACTTCCTGCCGATGCATGTCTAAACTGGATGTTTACAGACAAGTTCATTCCATTATTAG  
-----+-----+-----+-----+-----+  
T S C R C M S K L D V Y R Q V H S I I R

541 ACGTTCCCTGCCAGCAACACTACCACAGTGTCTCAGGCAGCGAACAAGACCTGCCCCACCAA  
-----+-----+-----+-----+-----+  
R S L P A T L P Q C Q A A N K T C P T N

601 TTACATGTGGAATAATCACATCTGCAGATGCCCTGGCTCAGGAAGATTTTATGTTTTCCTC  
-----+-----+-----+-----+-----+  
Y M W N N H I C R C L A Q E D F M F S S

661 GGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCAACAAGGAGCT  
-----+-----+-----+-----+-----+  
D A G D D S T D G F H D I C G P N K E L

721 GGATGAAGAGACCTGTGAGTGTCTGCAGAGCGGGGCTTCGGCCTGCCAGCTGTGGACC  
-----+-----+-----+-----+-----+  
D E E T C Q C V C R A G L R P A S C G P

FIG. 2B

MATCH WITH FIG. 2C



MATCH WITH FIG. 2B

781 CCACAAAGAACTAGACAGAAACTCATGCCAGTGTGTCTGTAAAAACAACCTCTTCCCCAG  
-----+-----+-----+-----+-----+  
H K E L D R N S C Q C V C K N K L F P S

841 CCAATGTGGGGCCCAACCGAGAAATTGATGAAAAACACATGCCAGTGTGTATGTAAAAAGAAC  
-----+-----+-----+-----+-----+  
Q C G A N R E F D E N T C Q C V C K R T

901 CTGCCCCAGAAATCAACCCCTAAATCCTGGAAAATGTGCCCTGTGAATGTACAGAAAGTCC  
-----+-----+-----+-----+-----+  
C P R N Q P L N P G K C A C E C T E S P

961 ACAGAAATGCTTGTAAAAAGGAAAGAGTTCCACCACCAACATGCAGCTGTACAGACG  
-----+-----+-----+-----+-----+  
Q K C L L K G K K F H H Q T C S C Y R R

1021 GCCATGTACGAACCGCCAGAGGCTTGTGAGCCAGGATTTTCATATAGTGAAGAAGTGTG  
-----+-----+-----+-----+-----+  
P C T N R Q K A C E P G F S Y S E V C

1081 TCGTGTGTCCCTTCATATTTGGCAAAAGACCACAAATGAGCTAAGATTGTACTGTTTCCA  
-----+-----+-----+-----+-----+  
R C V P S Y W Q R P Q M S \*

FIG. 2C

MATCH WITH FIG. 2D

MATCH WITH FIG. 2C

1141 GTTCATCGATTTTCTATTATGGA AAACTGTGTGTCACAGTAGAACTGTCTGTGAACAGA  
-----+-----+-----+-----+-----+-----+-----+  
1201 GAGACCCCTTGTGGGTCCATGCTAACAAAGACAAAAGTCTGTCTTTCCCTGAACCATGTGGA  
-----+-----+-----+-----+-----+-----+-----+  
1261 TAACTTTACAGAAATGGACTGGAGCTCATCTGC AAAAGGCCCTCTTGTAAGACTGGTTTT  
-----+-----+-----+-----+-----+-----+-----+  
1321 CTGCCAATGACCAACAGCCCAAGATTTTCCCTCTTG TGATTTCTTTAAAGAAATGACTATA  
-----+-----+-----+-----+-----+-----+-----+  
1381 TAATTATTTC CACTAAAAATATGTTTCTGCATTCATTTTATAGCAACAACAATGGT  
-----+-----+-----+-----+-----+-----+-----+  
1441 AAAACTCACTGTGATCAATATTTTATATCATGC AAAAATATGTTTAAAAATGAAAA  
-----+-----+-----+-----+-----+-----+-----+  
1501 TTGTATTATAAAAAA AAAAAA  
-----+-----+-----+-----+-----+-----+-----+

FIG. 2D

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1 50  
Pdga .MRTLACLLL LCCYLALVL AEEAIPREV IERLARSQIH SIRDLORLLE  
Pdgb MNRCWA.LFL SLCCYLRLVS AEGDPIPEEL YEMLSDHSIR SFDDLORLLH  
Vegf .....MNFL SWVHWSLALL LY..... .LHAKWSQA  
Vegf2 .....MTV LYPEYKMYK CQ..... .LRKCGWQH

51 100  
Pdga IDSVGSEDSL DTSRAHGVH ATKHVPEKRP LPIRRKRSI. ....EEAVP  
Pdgb GDP.GEEDGA ELDLNMTRSH SGGELES... .LARGRRSLG SLTIAEPAMI  
Vegf APMAE.....GGCQ NHHEVVKFMD .VYQR.....  
Vegf2 REQANLNSRT EETIKFAAH YNTEILKSID NEWRK.....

101 150  
Pdga AVCKTRTVIY EIPRSQVDPT SANFLIWPPC VEVKRC TGCC NTSSVKCQPS  
Pdgb AECKTRTEVF EISRRIDRT NANFLVWPPC VEVQRC SGCC NNRNVCQRP  
Vegf SYCHPIETLV DIFQYDPI .EYIFKPS VPLMRCCGCC NDEGLEQPT  
Vegf2 TOCMPREVCI DVGKEFGVAT ..NTFFKPPC VSVYRCGCC NSEGLQCMNT

151 200  
Pdga RVHHRVKVA KVEYVRKKPK LKEVQRLEE HLEQAC..... AT.....  
Pdgb QVQLRPVQVR KIEIVRKKPI FKCATVTLED HLAQC..... ETVAARPVT  
Vegf EESNITMQIM RIK.PH..QG QHIGEMSFLQ HNKCEORPKK DRARQEKKS  
Vegf2 STSYLSKTLF EIT.VPLSQG PKPVTISFAN HTSCROMSKL DVYRQVHSII

FIG. 3A

201 250  
Pdgha ..... TSLNPD YREEDTDVR.  
Pdghb RSPGGSQEQ AKTPQTRVTI RTVRVRRPPK GKHRKFHHTH DKTALKETLG  
Vegf RGK..... GKQKRRK KSRYSWSVY VGARCCMPW SLPQPHF  
Vegf2 RRSLPATLPQ COAANKTCPT NYMNNHICR CLAQEDFMFS SDAGDDSDTG

251 300  
Pdgha .....  
Pdghb A.....  
Vegf ..... CGP..... CSE RRKHLFVQDP QTCKCCKNT  
Vegf2 FHDICGNKE LDEETCCVC RAGLRPASCG PHKEL...DR NSCQCVCKNK

301 350  
Pdgha .....  
Pdghb .....  
Vegf ..... DSRCKARQ LELNERTCRC DKPRR.....  
Vegf2 LFPSQCCANR EFDENTCCQ VCKRTCPRNQ PLNPKKACE CTESPOKCLL

351 398  
Pdgha .....  
Pdghb .....  
Vegf .....  
Vegf2 KGKKFHHQTC SCYRRPCTNR QKACEPGFSY SEEVCRCPVS YWQRPQMS

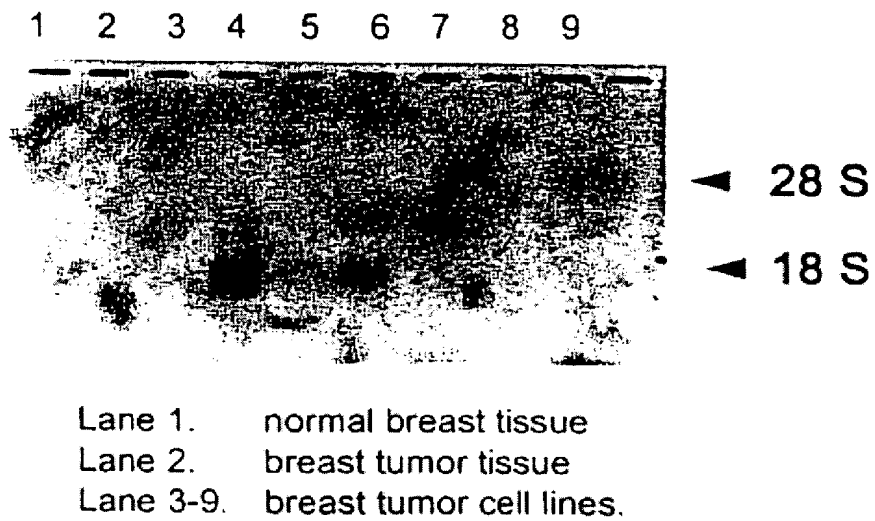
FIG. 3B

PERCENTAGE (%) OF AMINO ACID IDENTITIES BETWEEN  
 EACH PAIR OF GENES IS SHOWN IN THE  
 FOLLOWING TABLE

	PDGF $\alpha$	PDGF $\beta$	VEGF	VEGF-2
PDGF $\alpha$				
PDGF $\beta$	48.0			
VEGF	20.7	22.7		
VEGF-2	23.5	22.4	30.0	

FIG. 4

### Expression of VEGF2 mRNA in Human Breast Tumor Cells



**FIG. 5**

## Expression of VEGF-2 mRNA in Human Adult Tissues

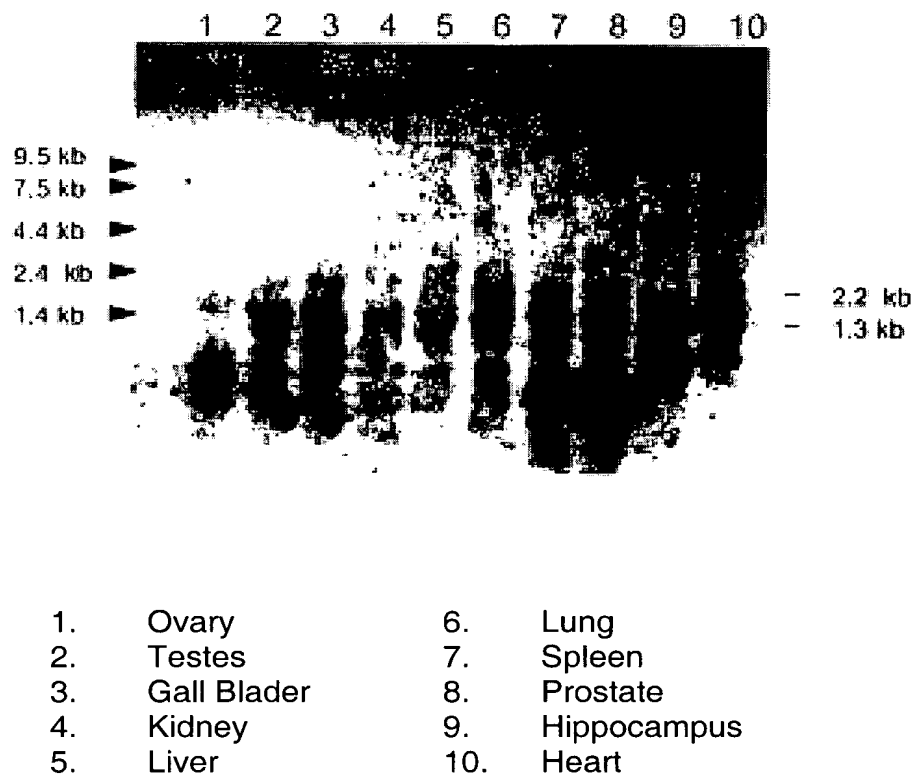
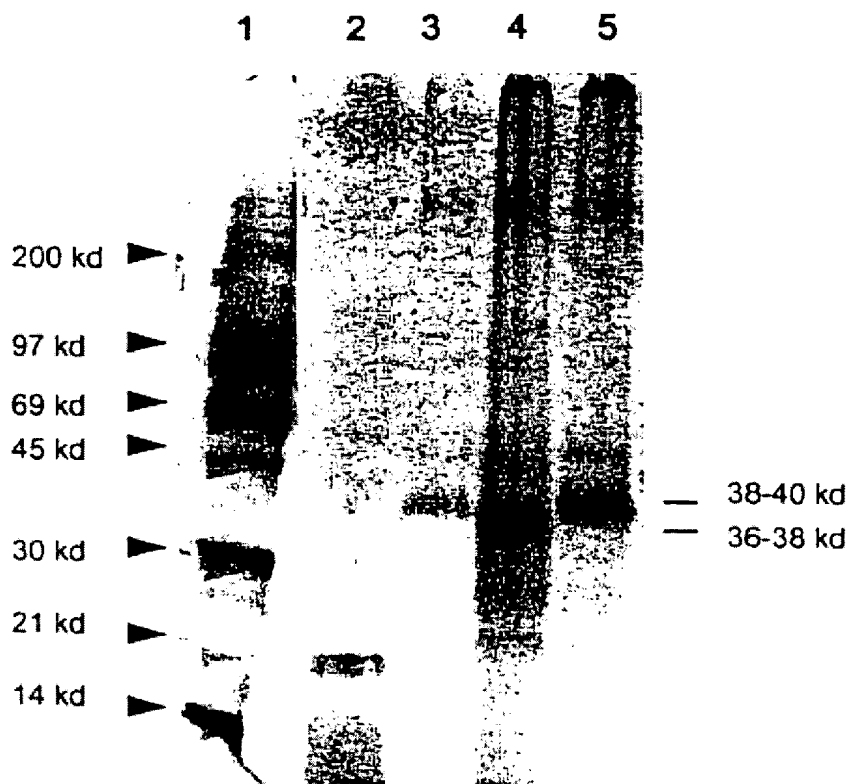


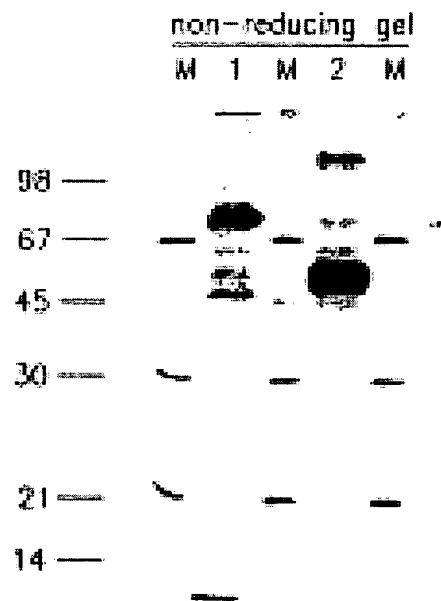
FIG. 6



- Lane 1: 14-C and rainbow M.W. marker  
Lane 2: FGF control  
Lane 3: VEGF2 (M13-reverse & forward primer)  
Lane 4: VEGF2 (M13-reverse & VEGF-F4 primer)  
Lane 5: VEGF2 (M13-reverse & VEGF-F5 primer)

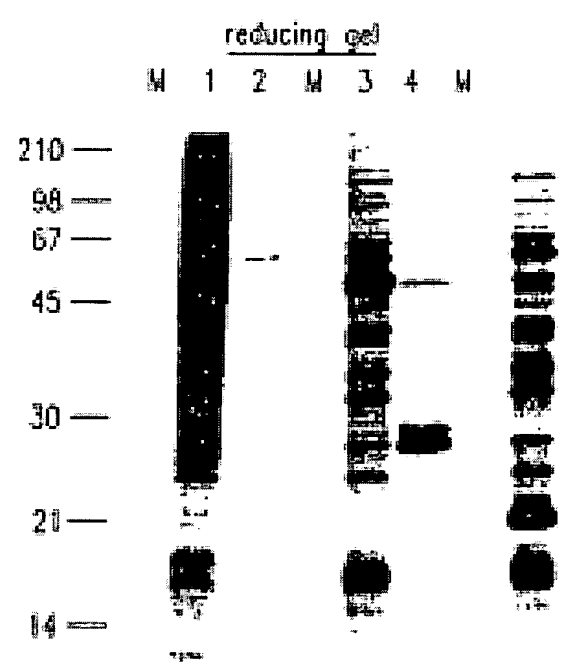
**FIG. 7**





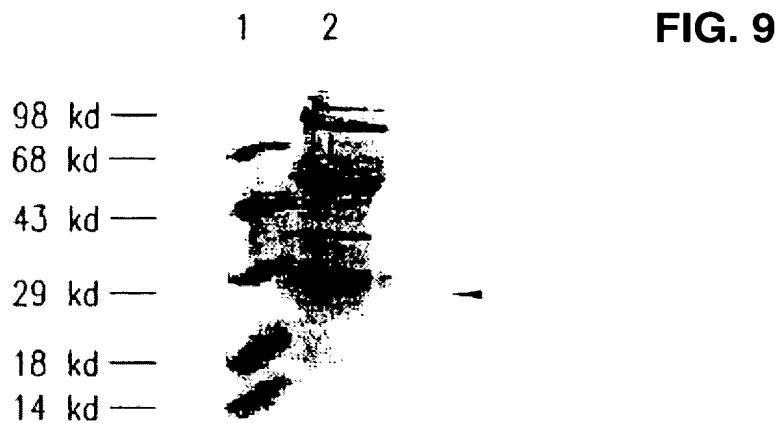
Lane M: Marker  
Lane 1: Vector medium  
Lane 2: VEGF2 medium

FIG. 8A

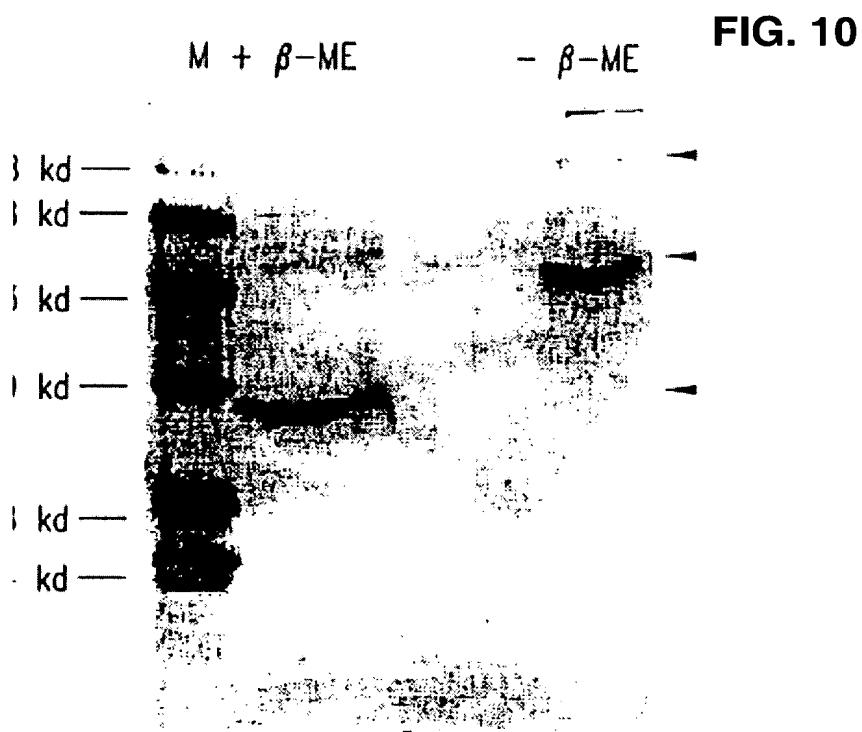


Lane M: Marker  
Lane 1: vector cytoplasm  
Lane 2: vector medium  
Lane 3: VEGF2 cytoplasm  
Lane 4: VEGF2 medium

FIG. 8B



Lane 1: Molecular weight marker  
Lane 2: Precipitates containing VEGF2.



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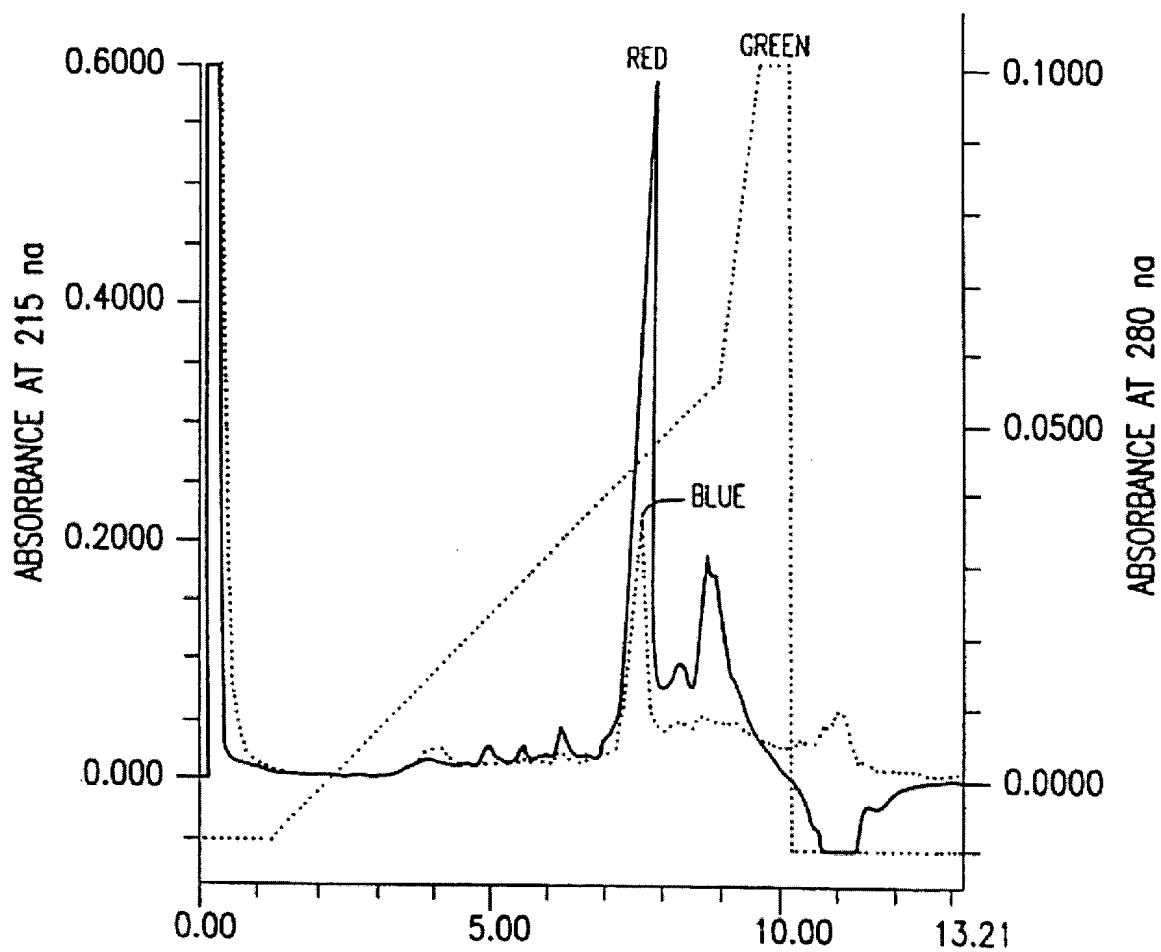


FIG. 11

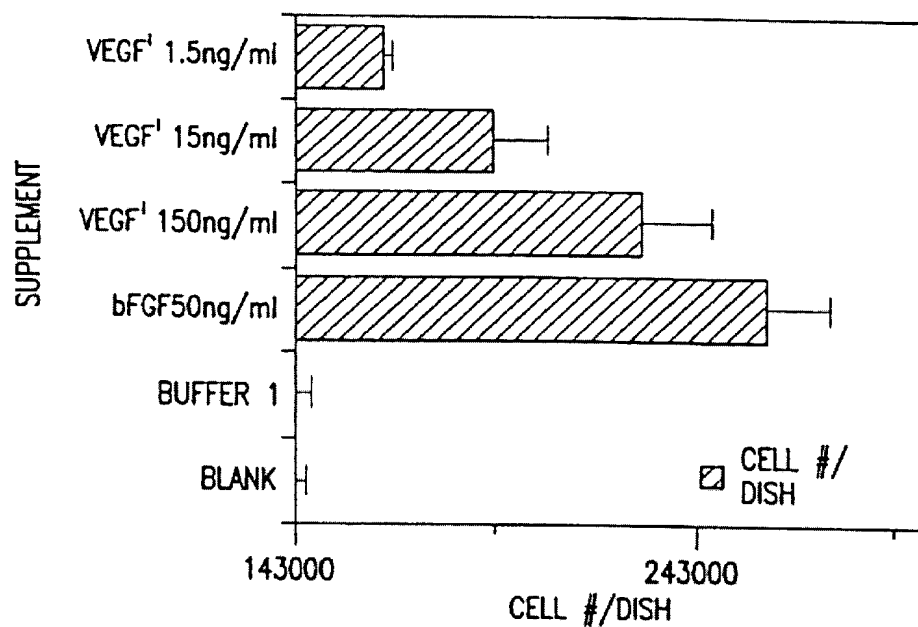


FIG. 12

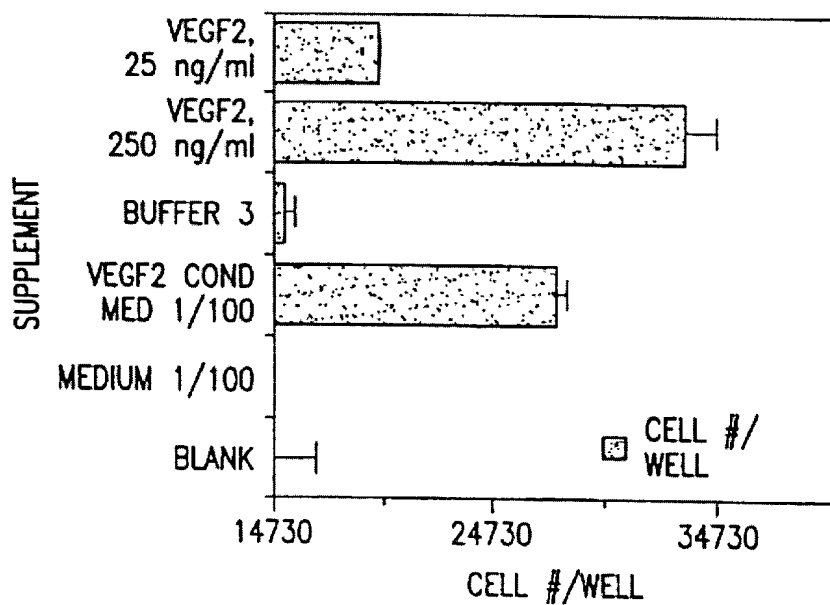


FIG. 13

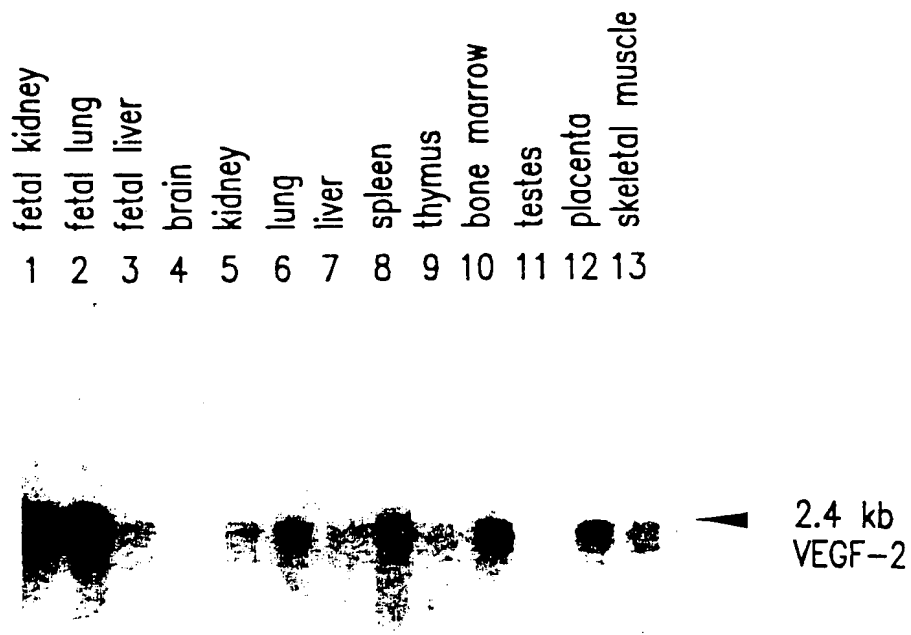


FIG. 14A

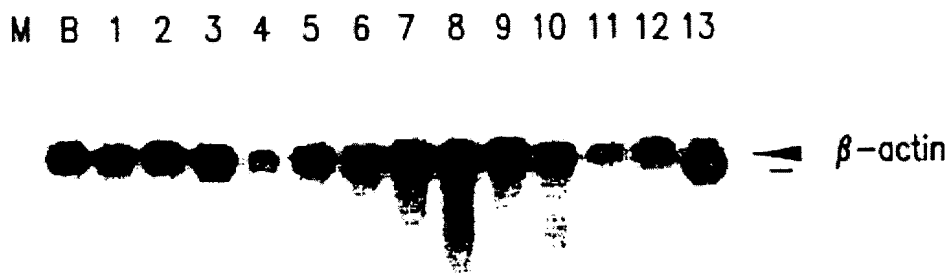


FIG. 14B

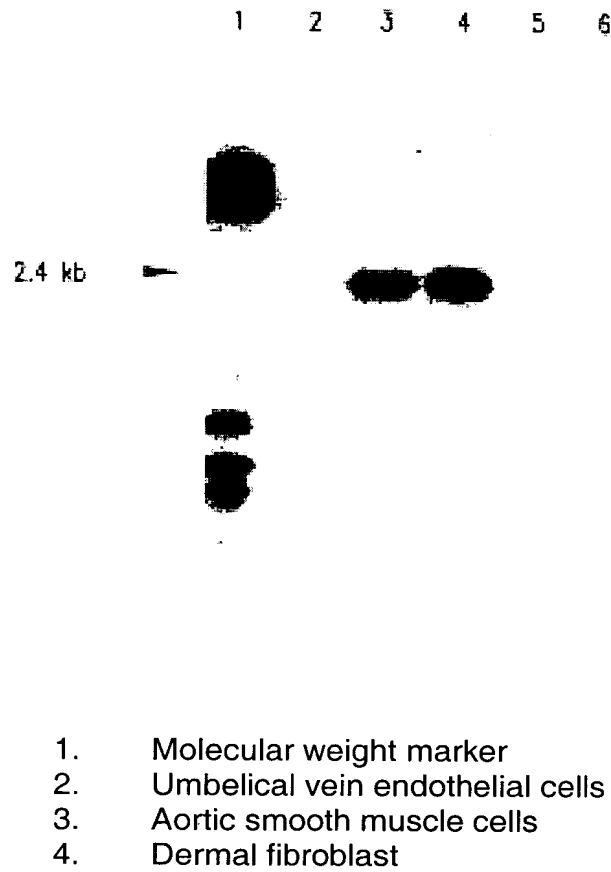
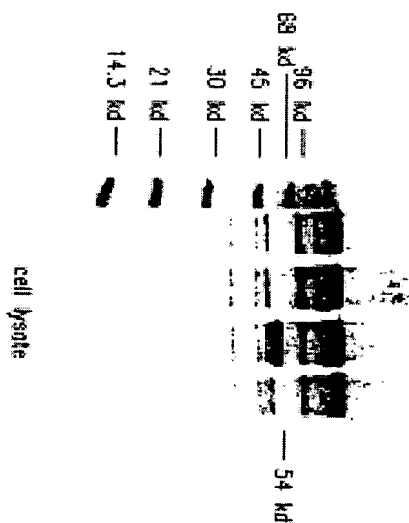


FIG. 15



1. Molecular weight marker
2. Blank
3. Control protein-HA
4. Vector control
5. VEGF2-HA

FIG. 16A



1. Molecular weight marker
2. Blank
3. Control protein-HA
4. VEGF2-HA
5. Vector control

FIG. 16B



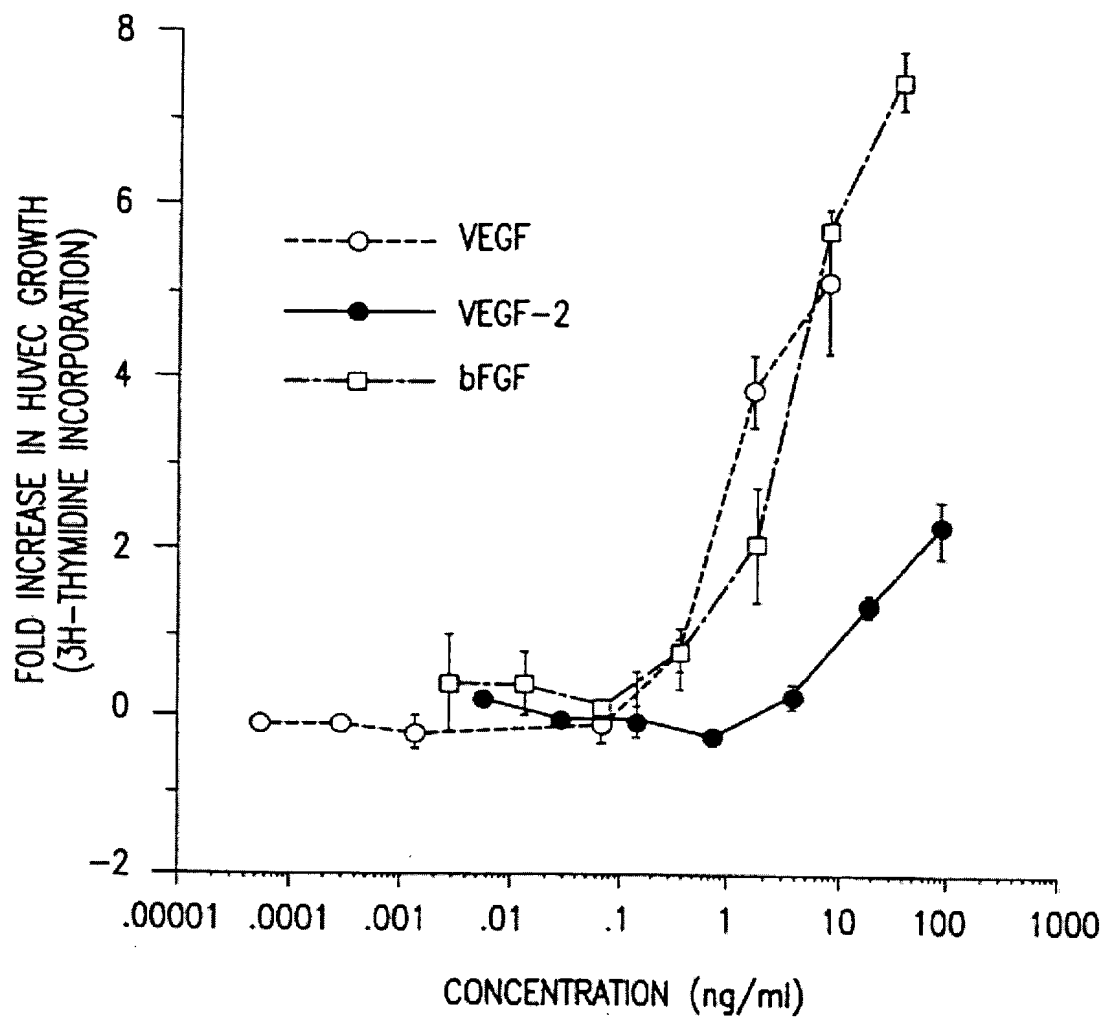


FIG. 17

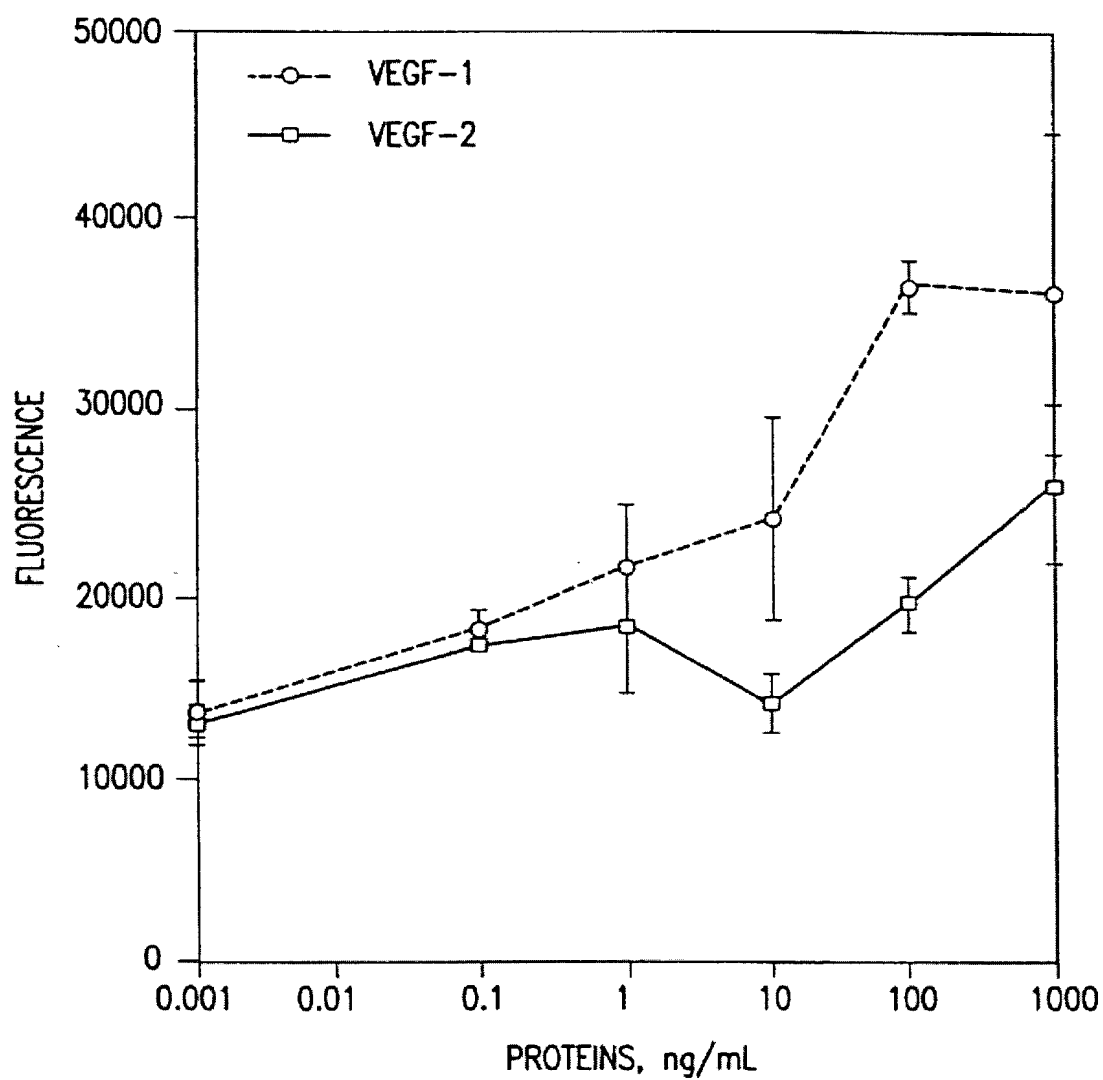


FIG. 18

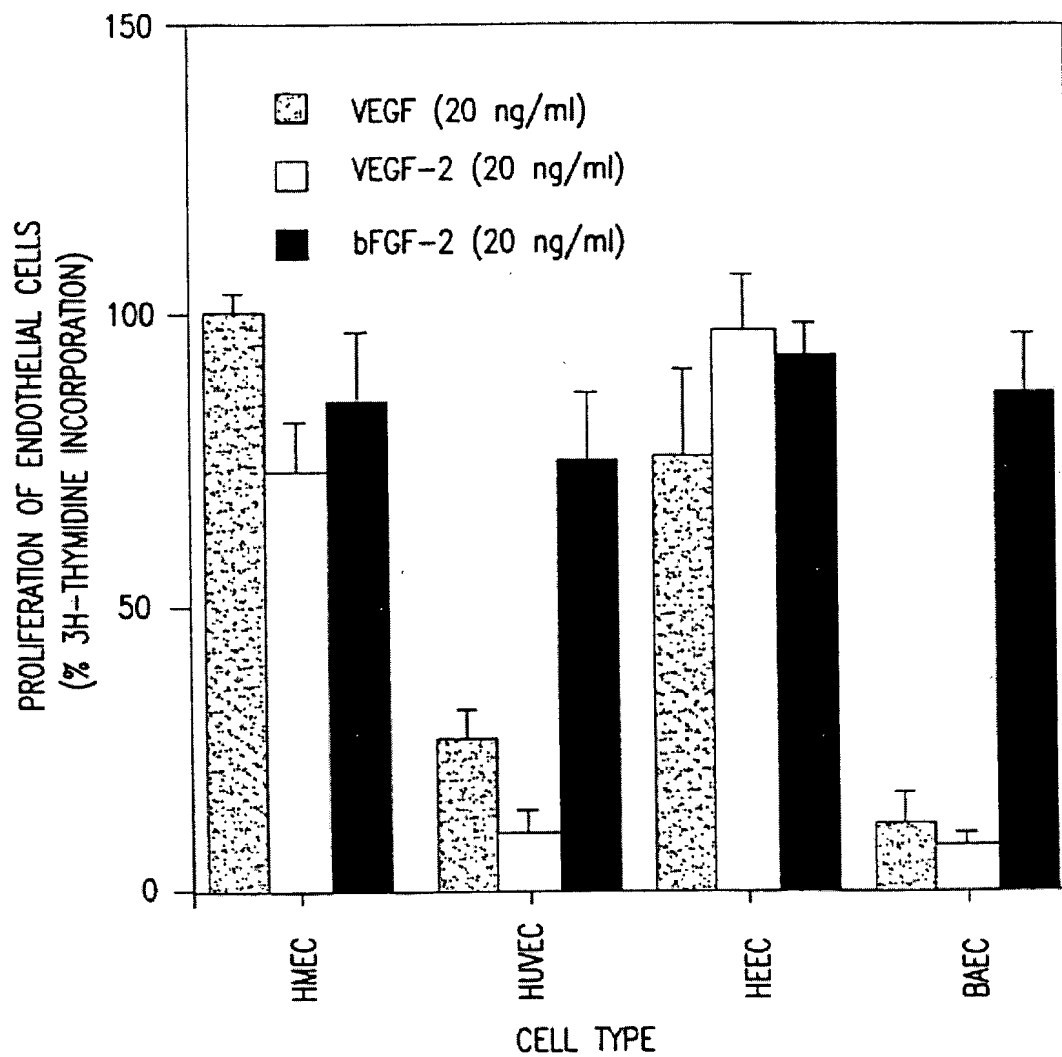


FIG. 19

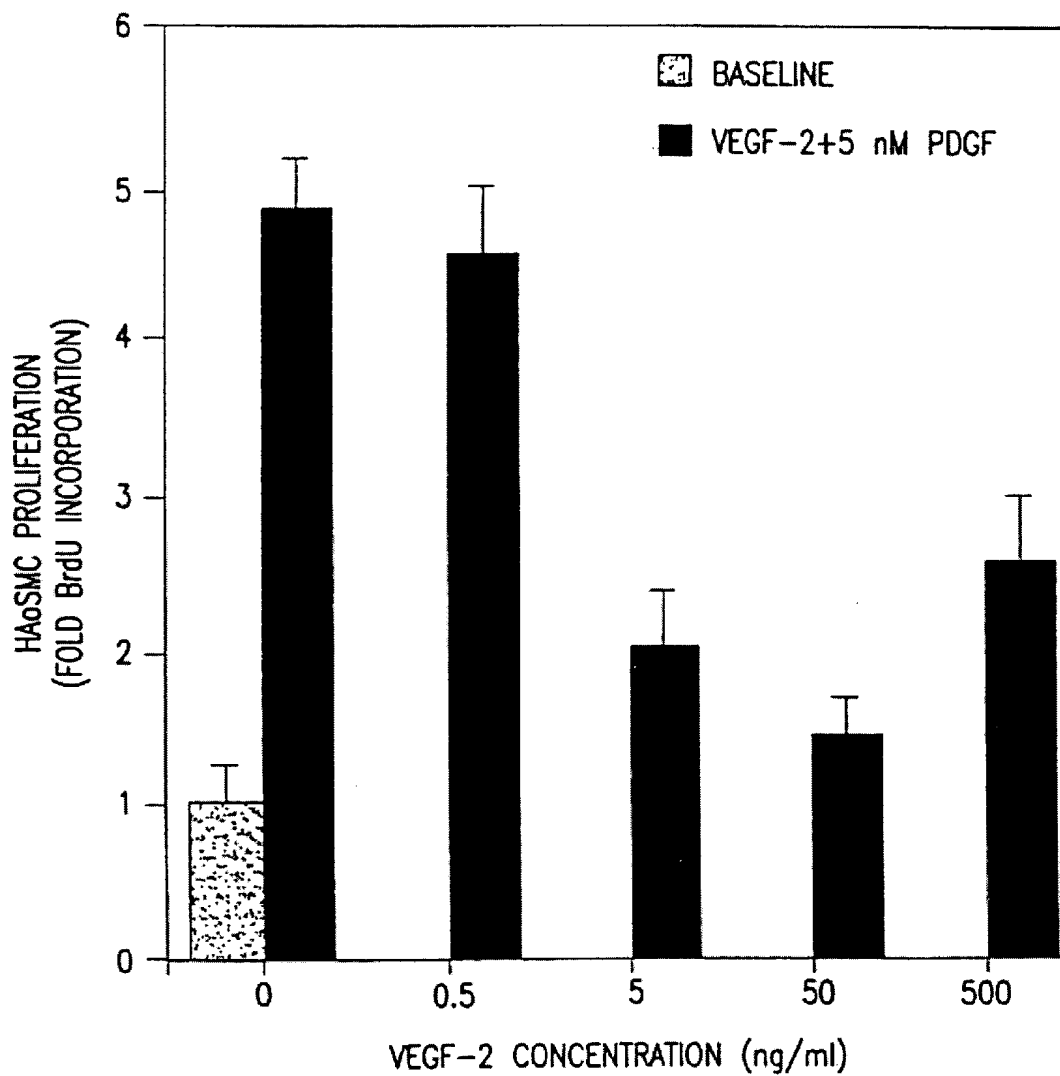


FIG. 20A

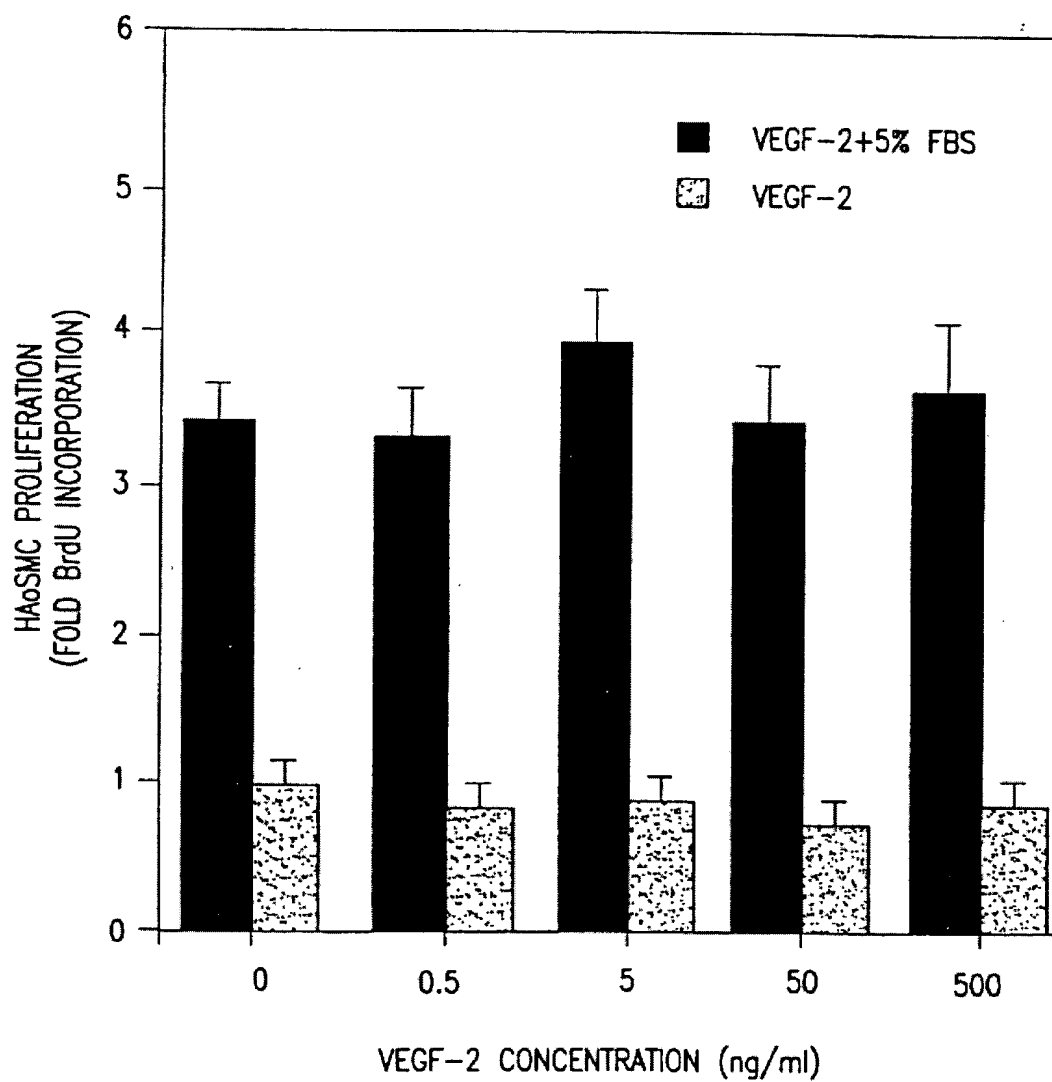


FIG. 20B

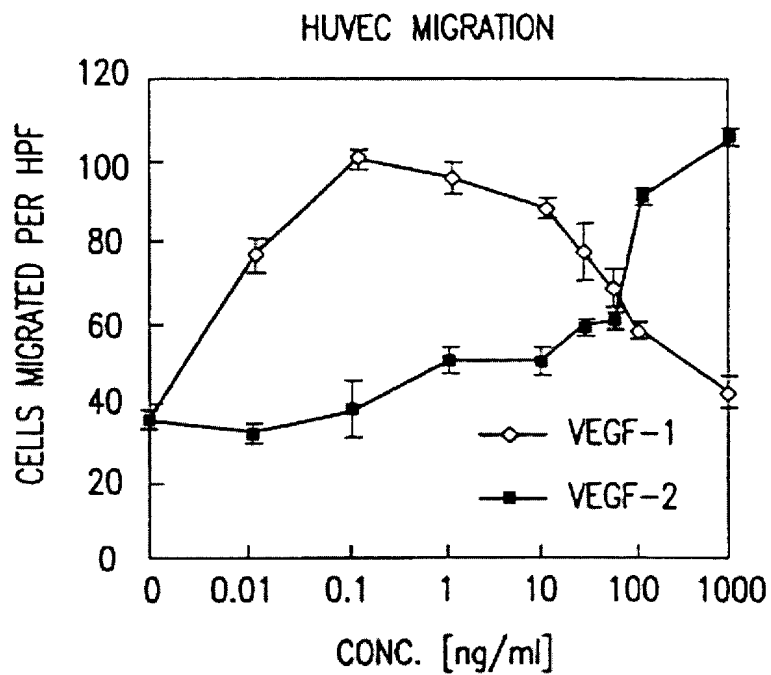


FIG. 21A

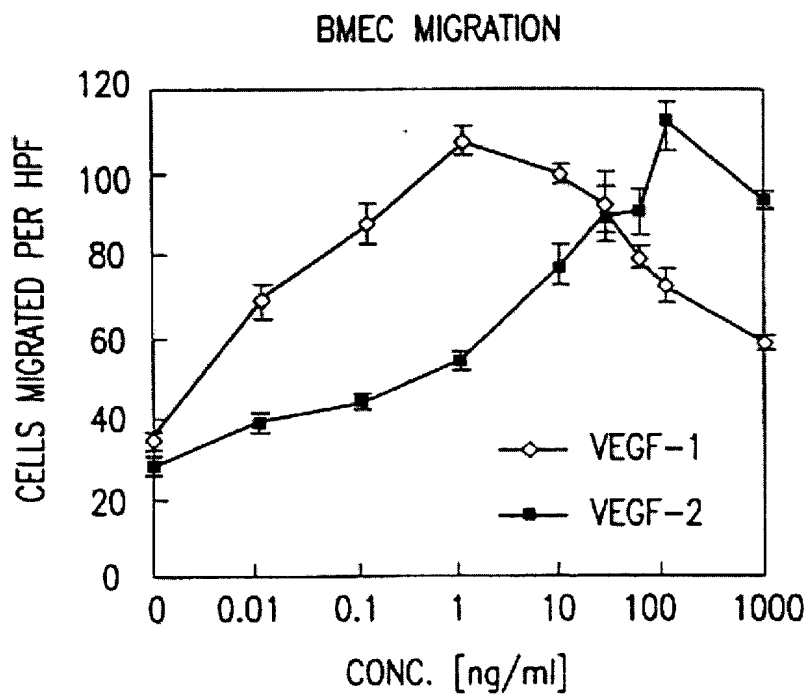


FIG. 21B

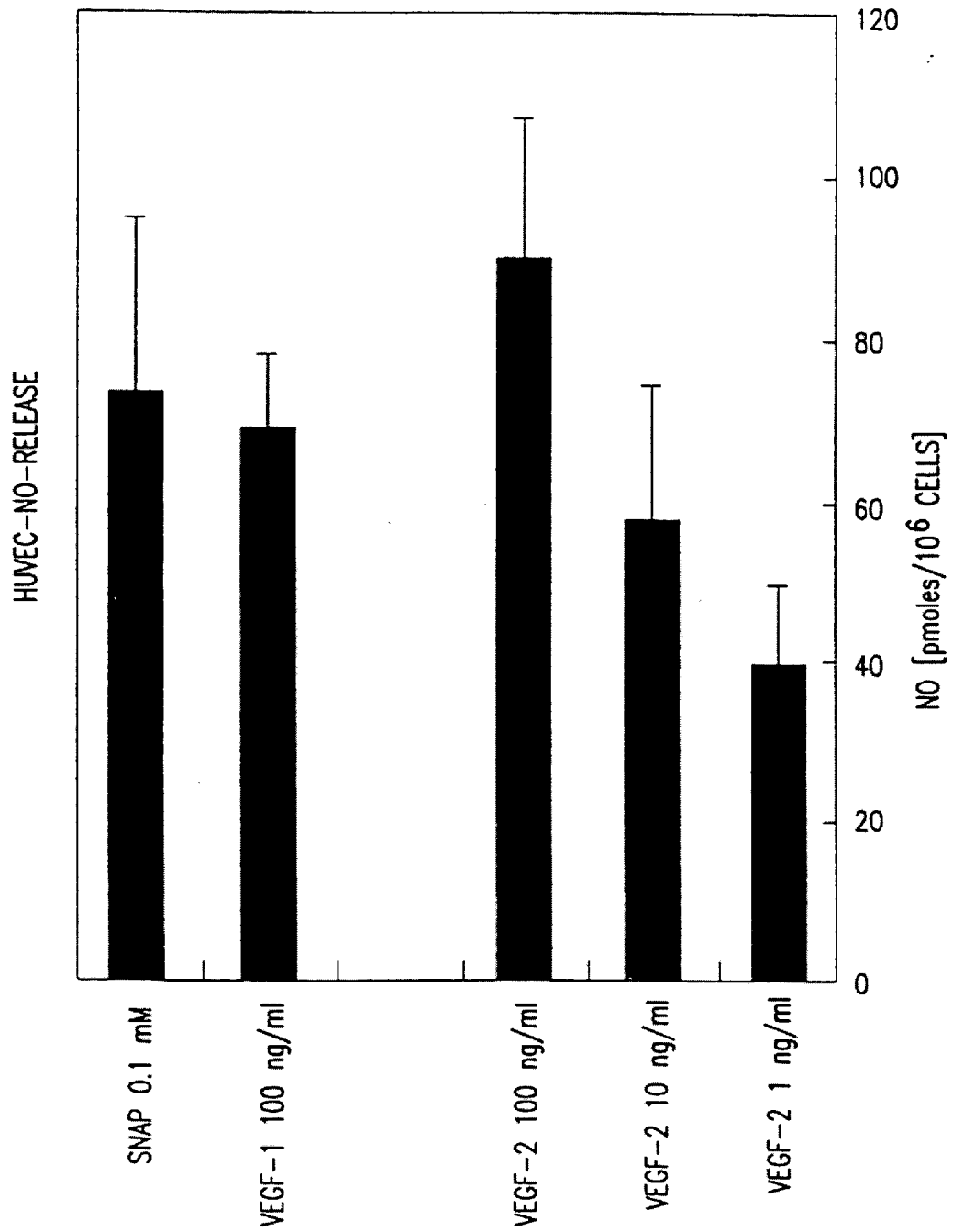


FIG. 22

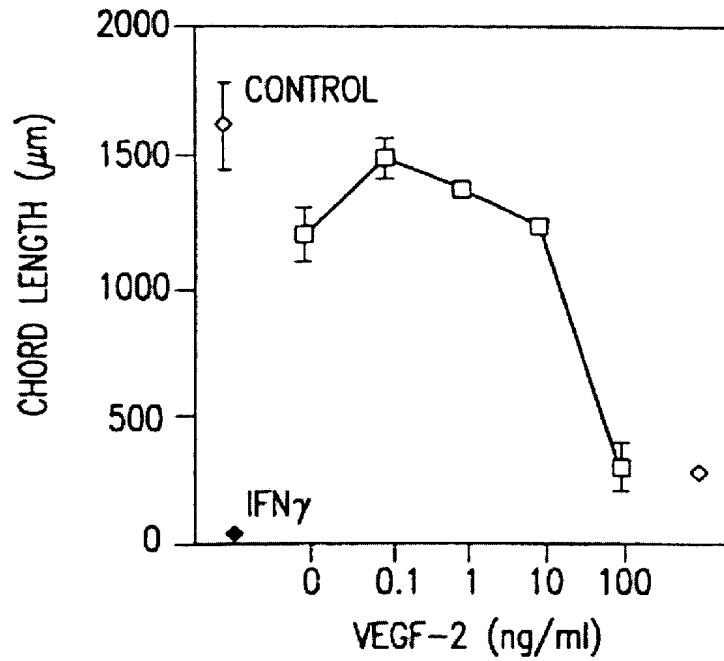


FIG. 23

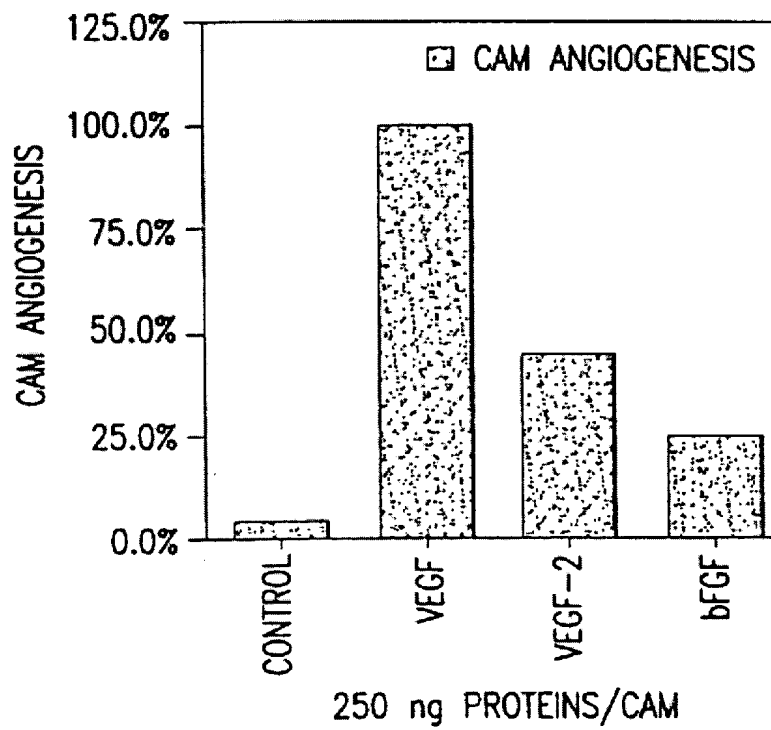


FIG. 24



CALF BLOOD PRESSURE RATIO  
-PROTEIN I.A.-

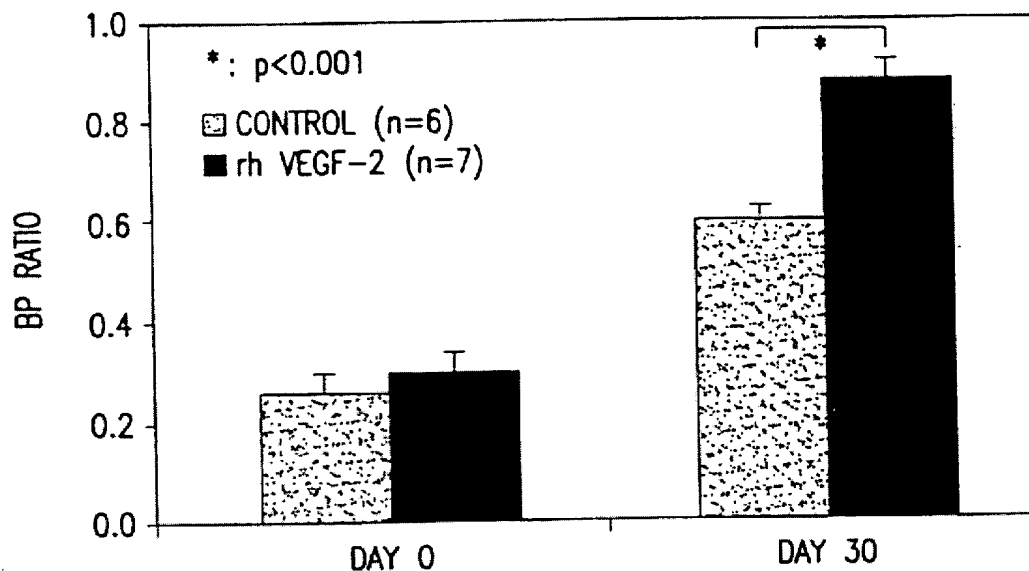


FIG. 25A

CALF BLOOD PRESSURE RATIO  
-PLASMID-

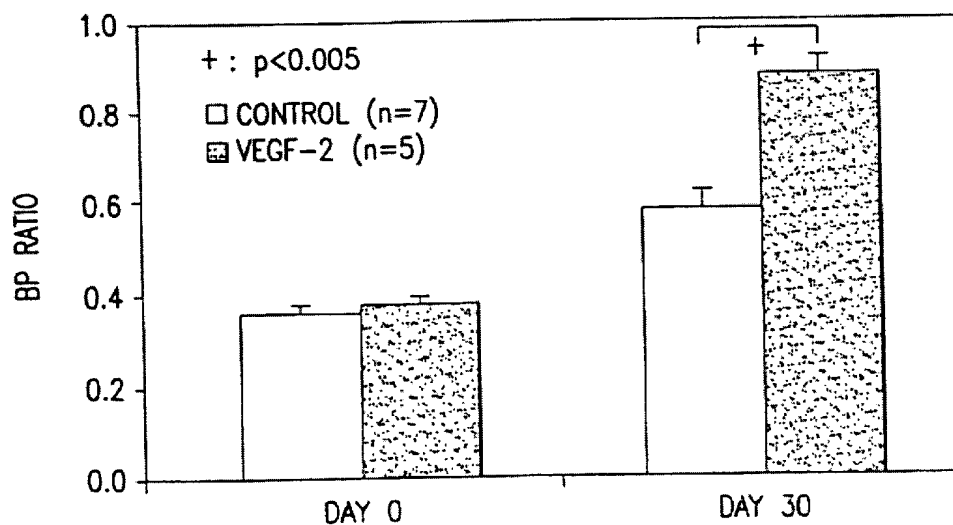


FIG. 25B

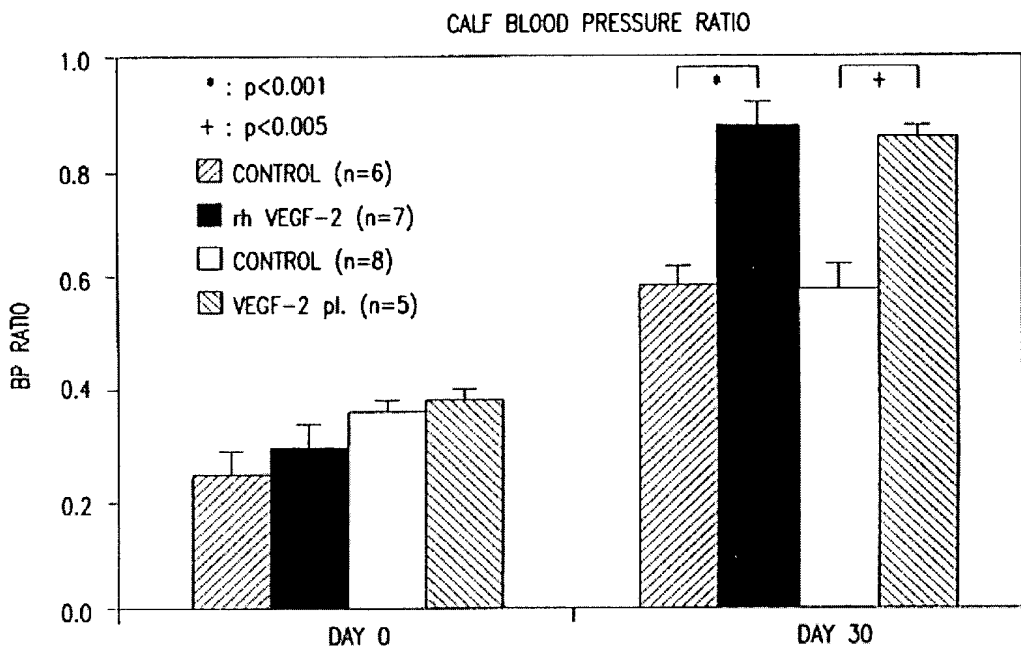


FIG. 25C

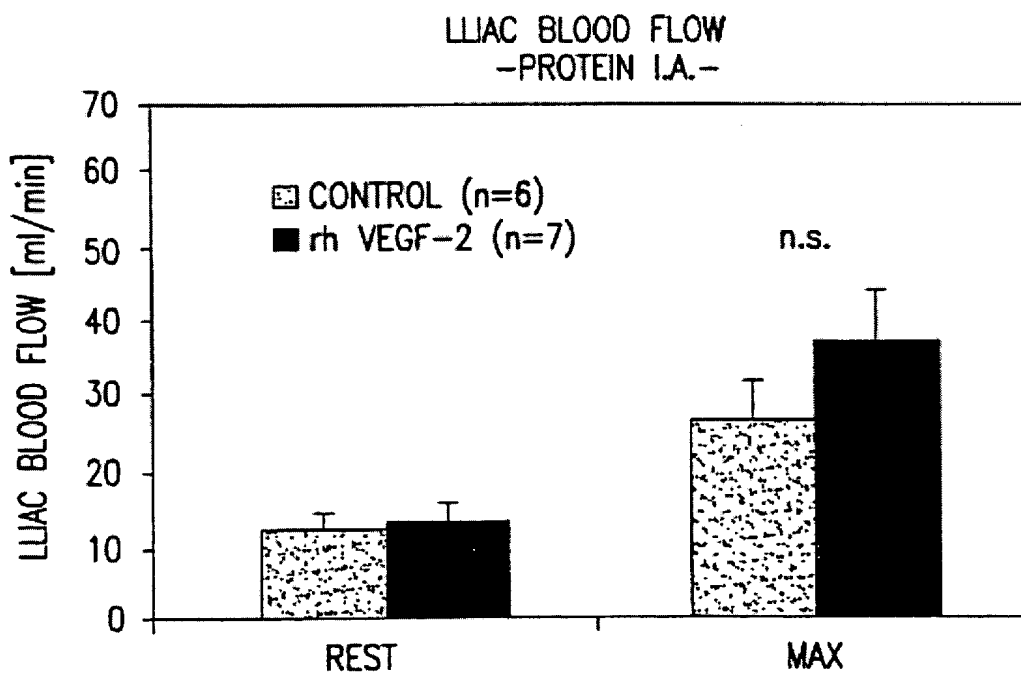


FIG. 25D

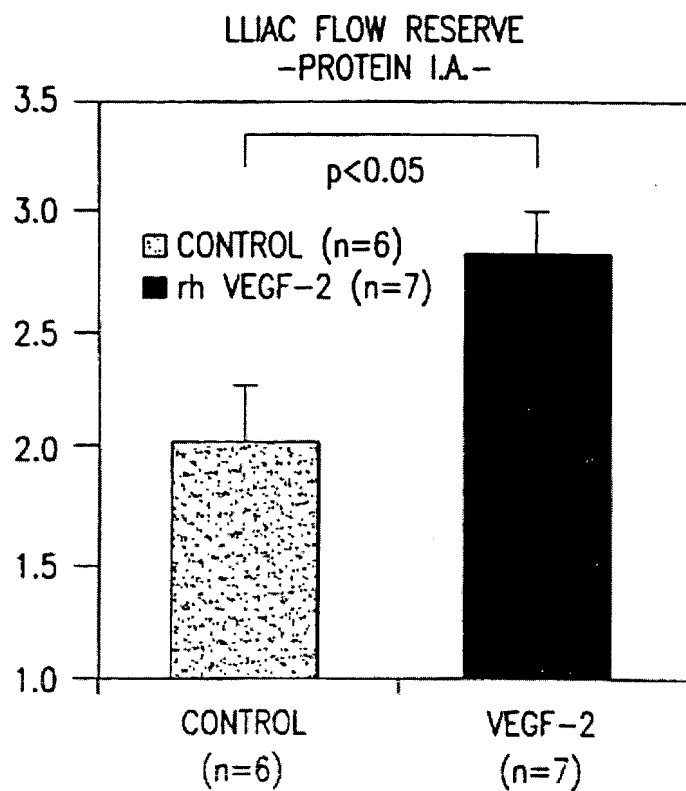


FIG. 25E

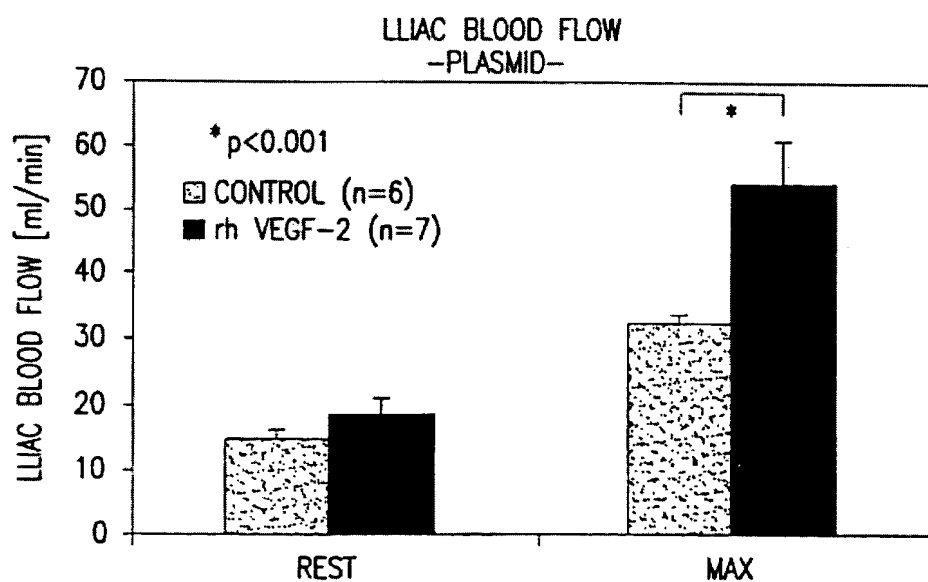


FIG. 25F

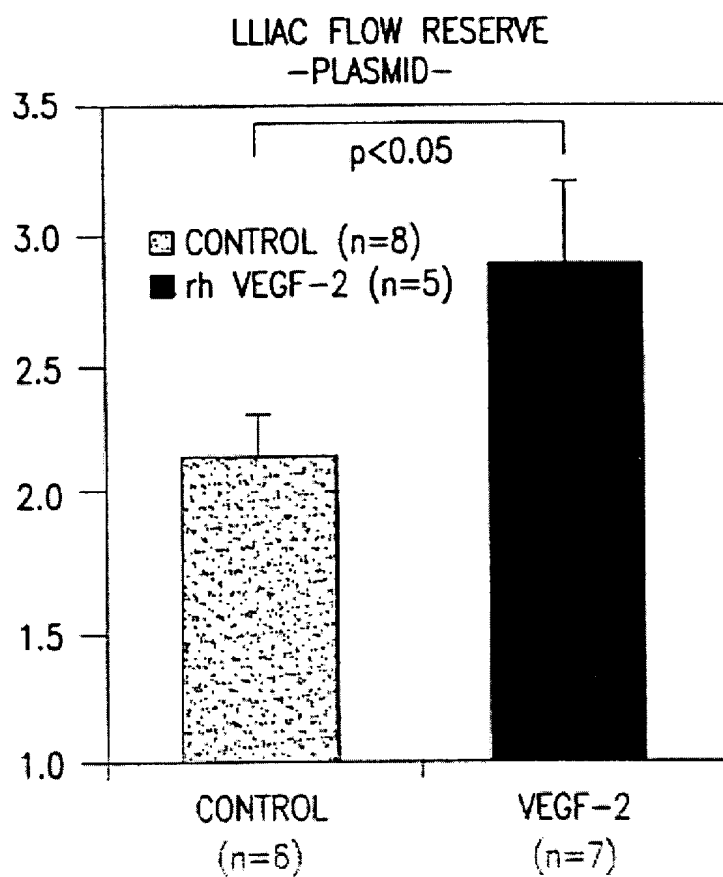


FIG. 25G

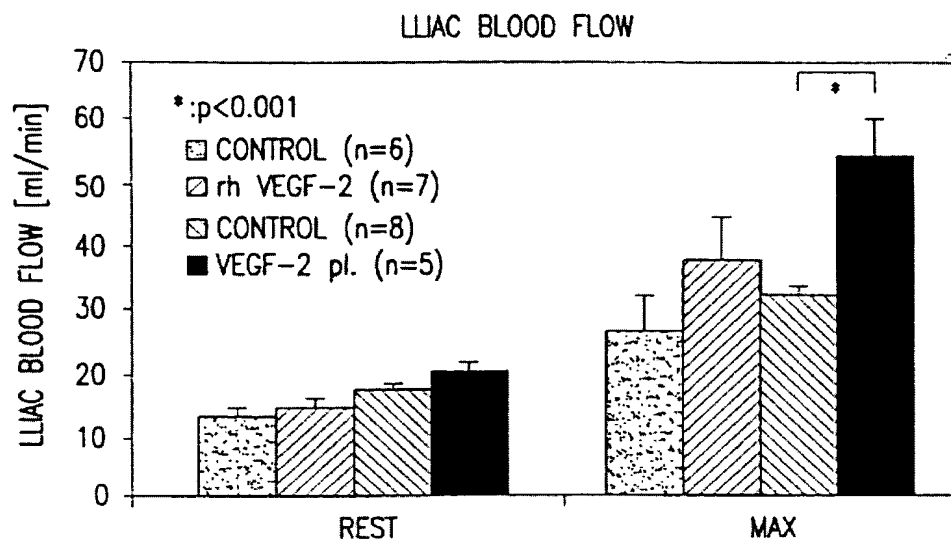


FIG. 25H

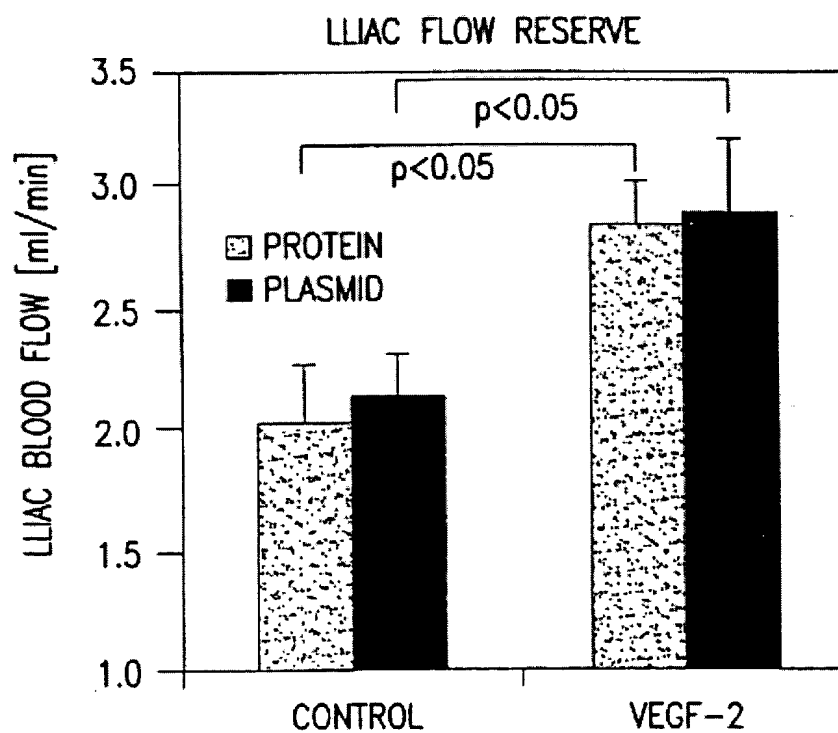


FIG. 25I

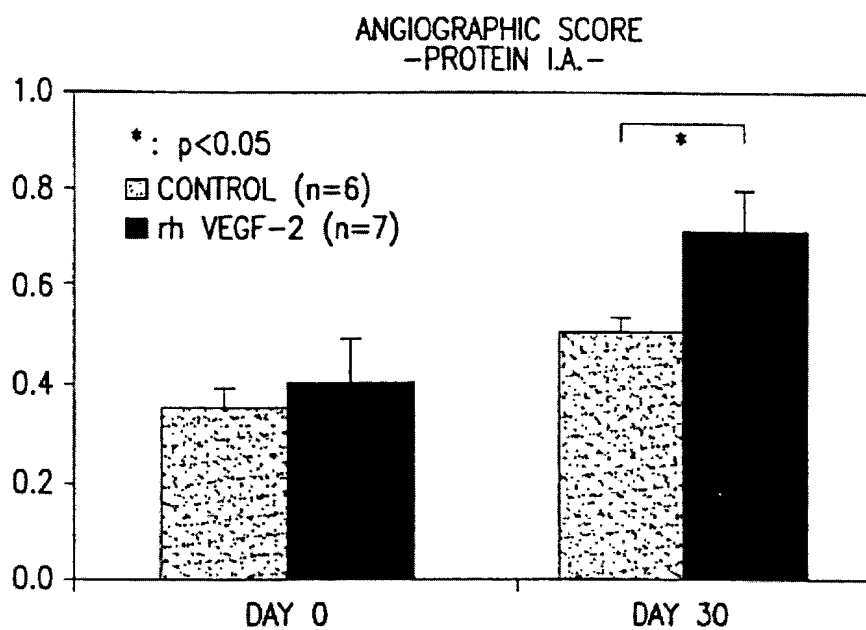


FIG. 25J

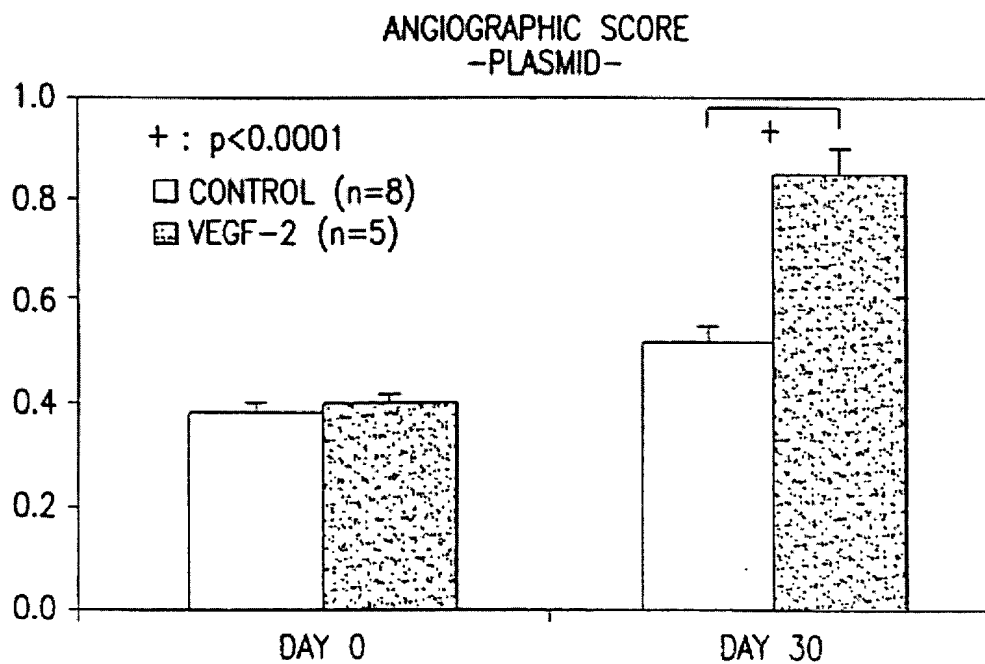


FIG. 25K

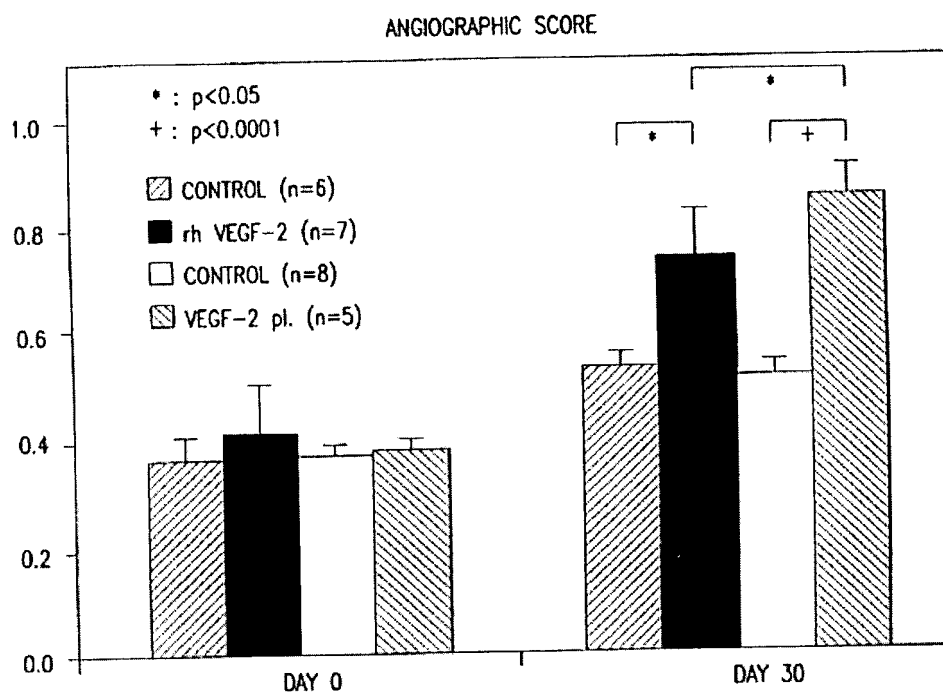


FIG. 25L

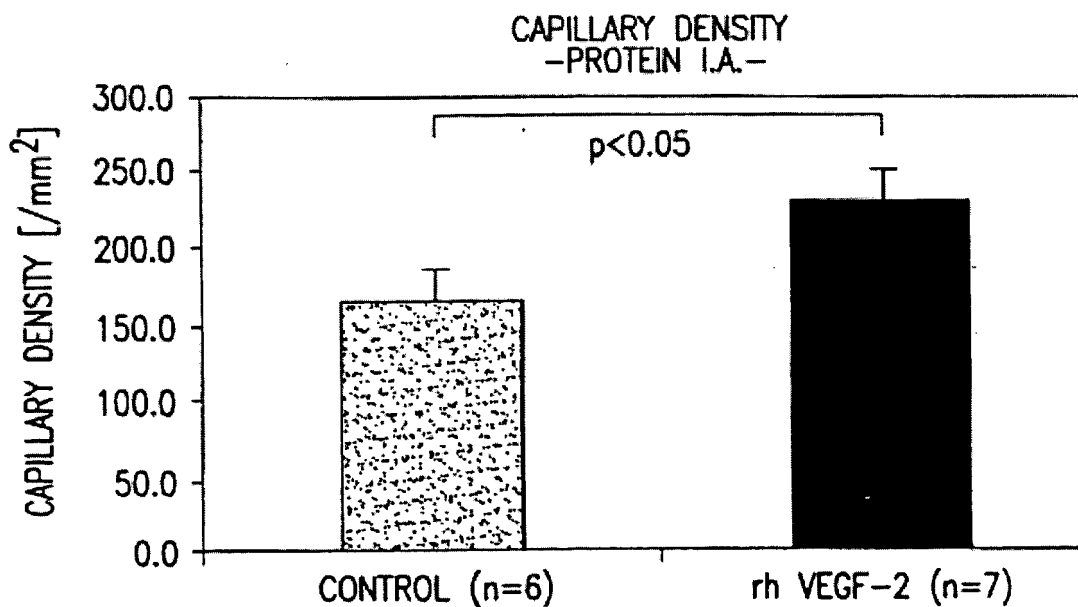


FIG. 25M

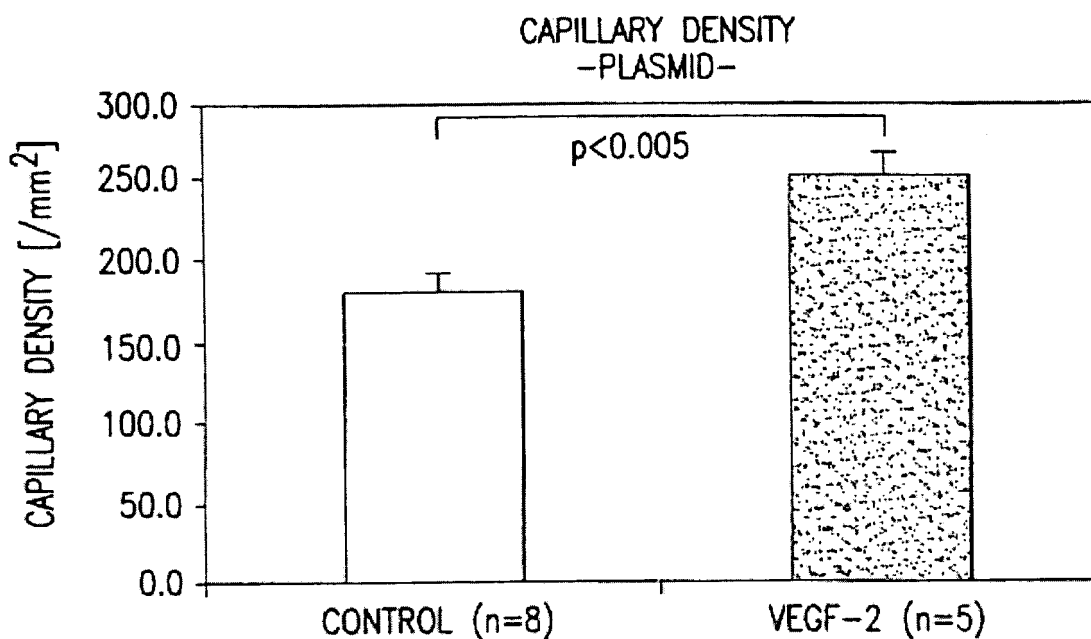


FIG. 25N

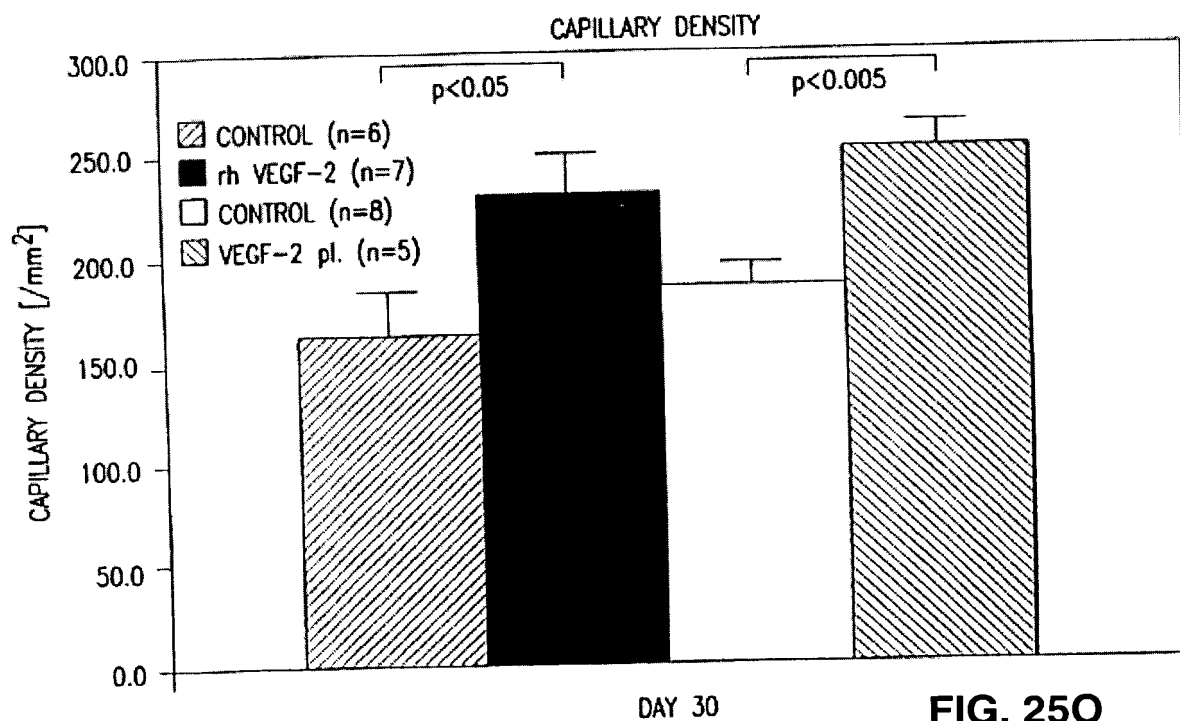


FIG. 25O



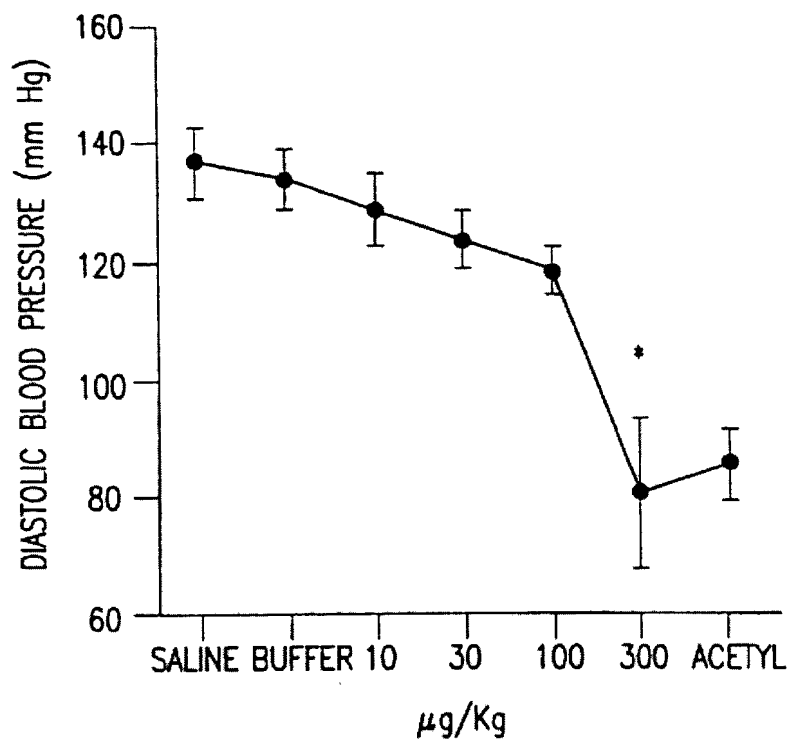


FIG. 26A

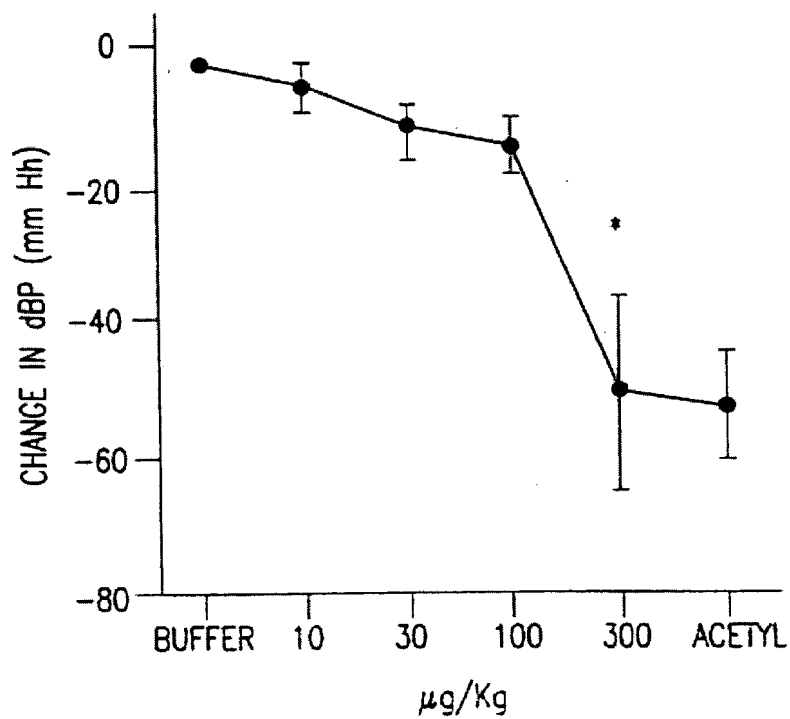


FIG. 26B

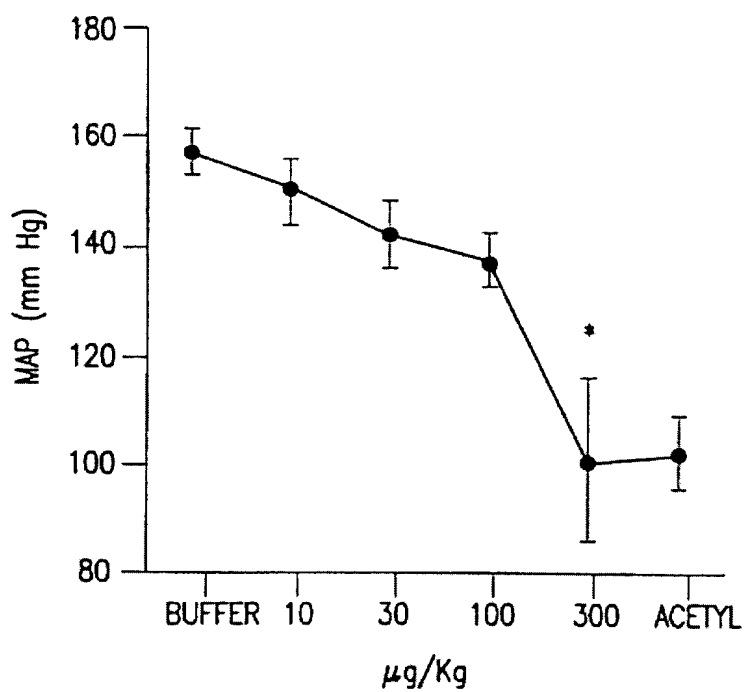


FIG. 26C

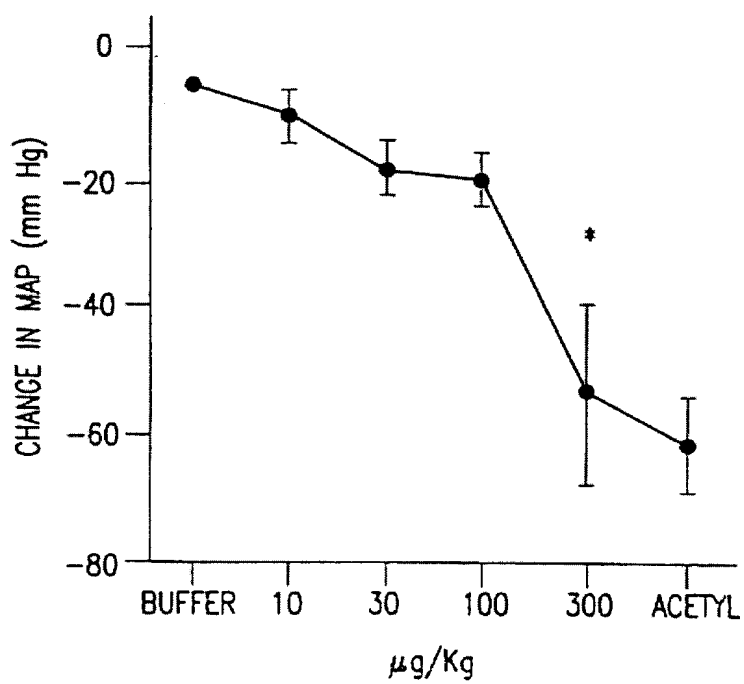


FIG. 26D

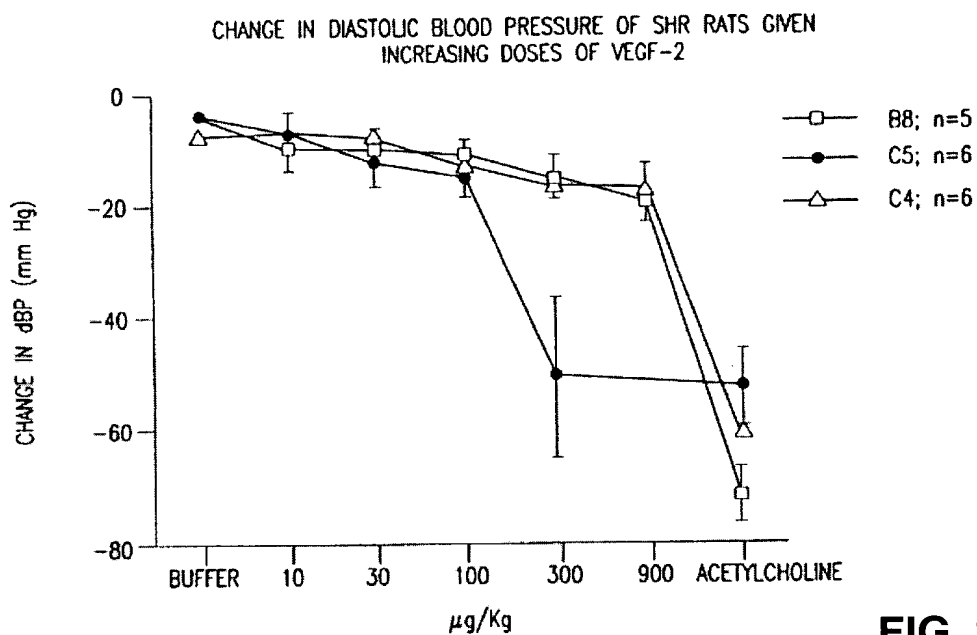


FIG. 26E

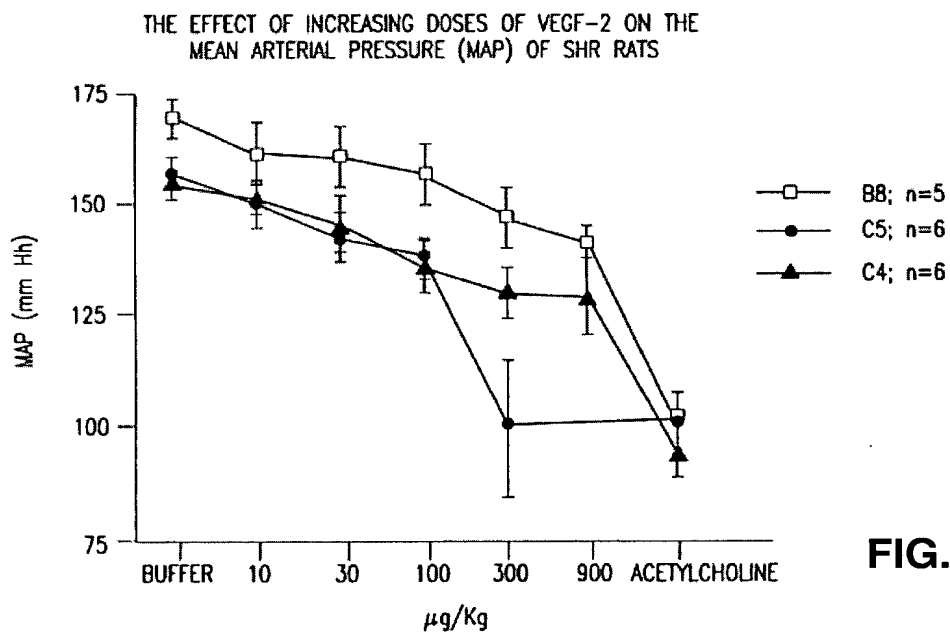


FIG. 26F

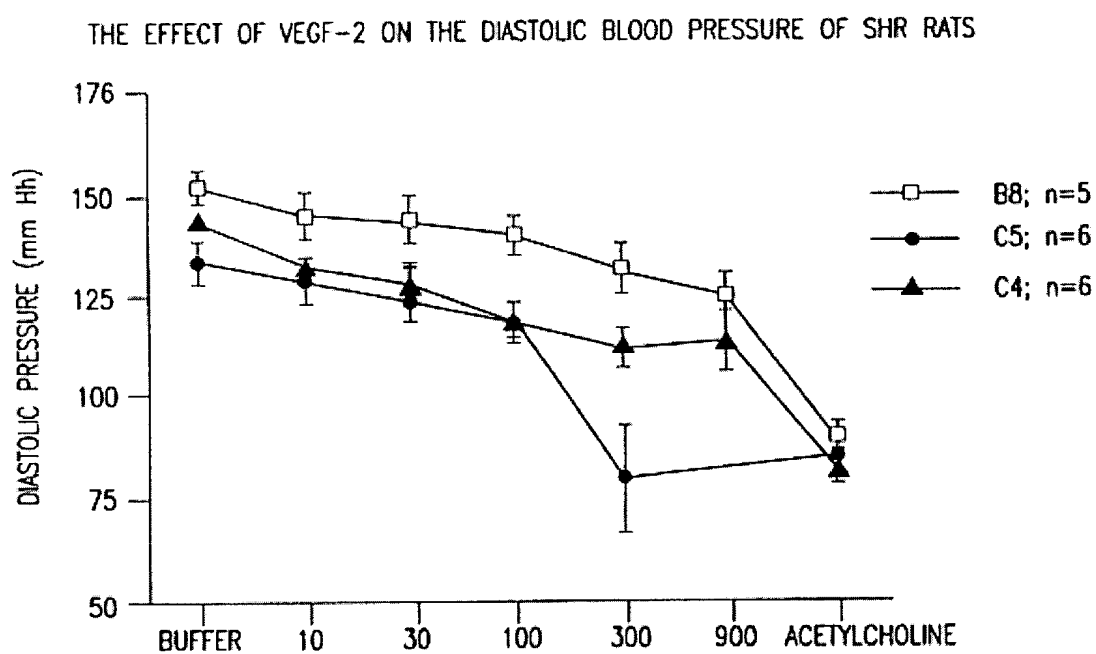


FIG. 26G

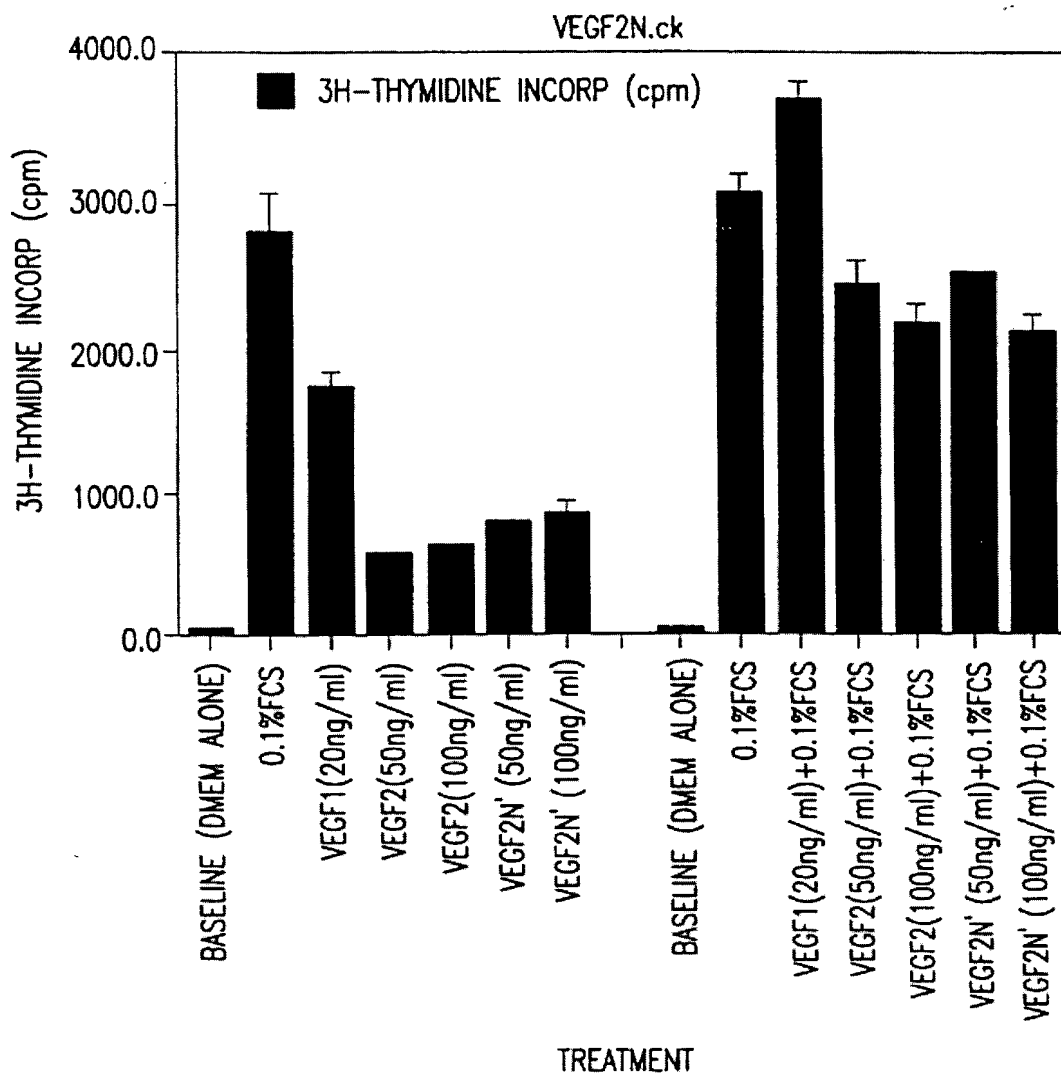


FIG. 27

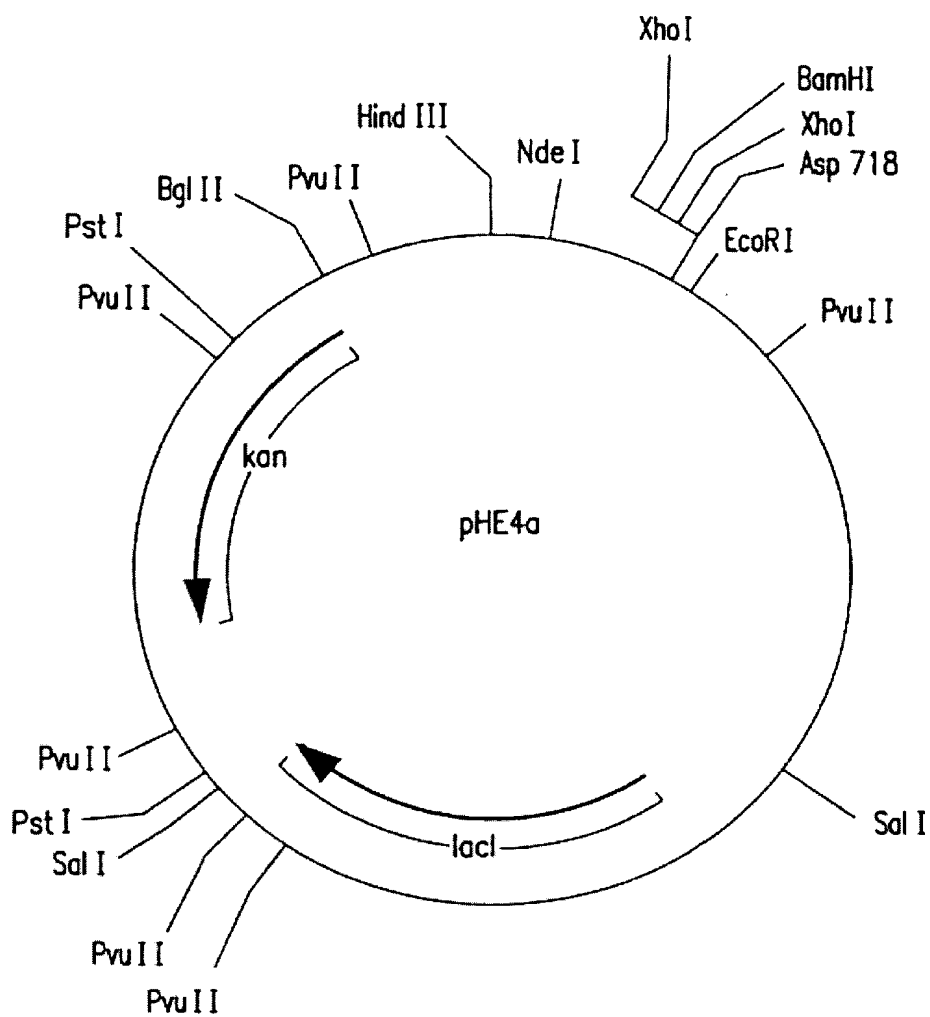


FIG. 28

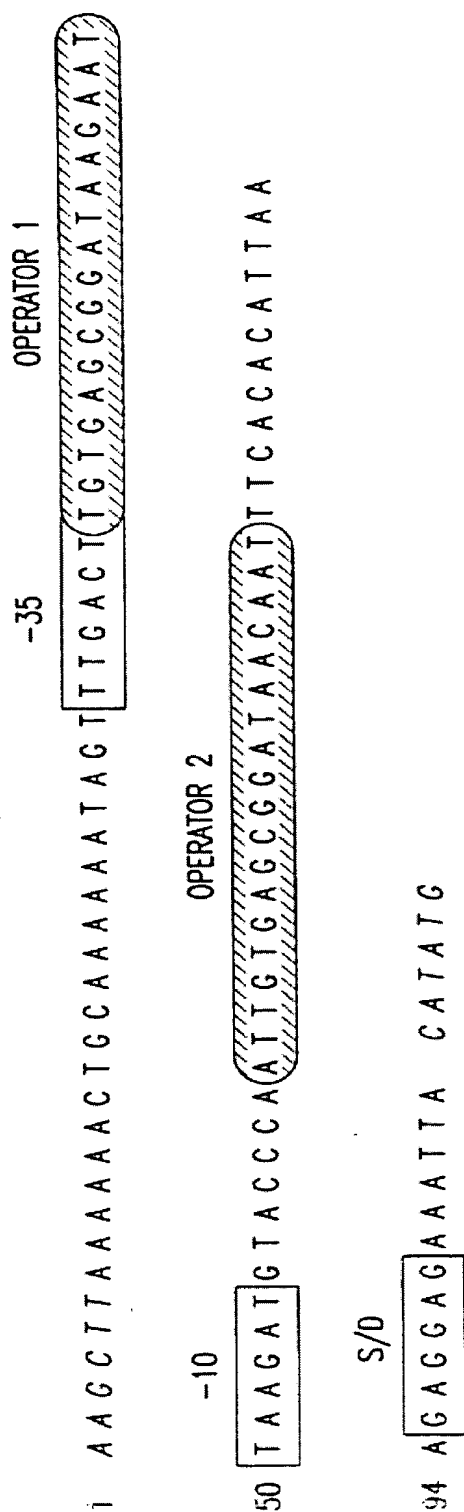


FIG. 29

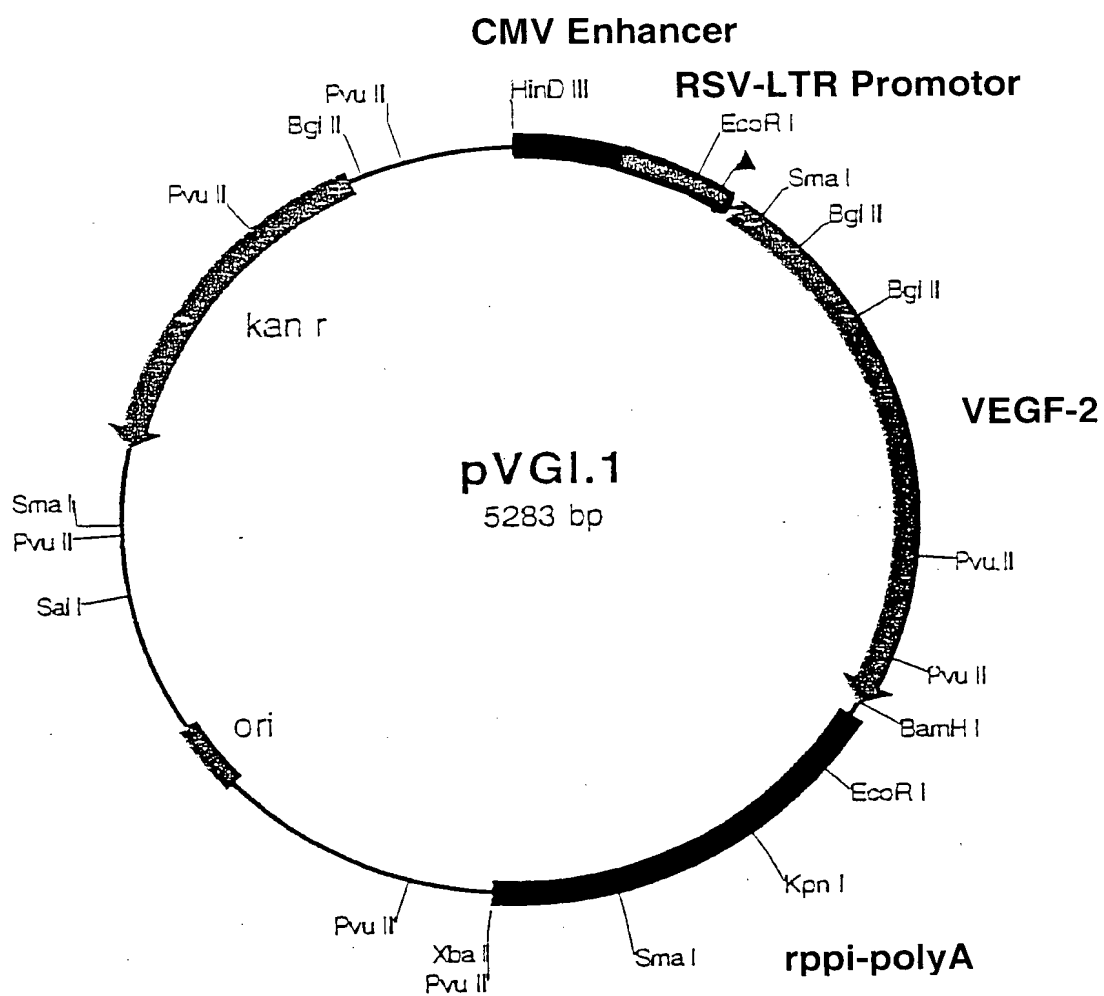


FIG. 30



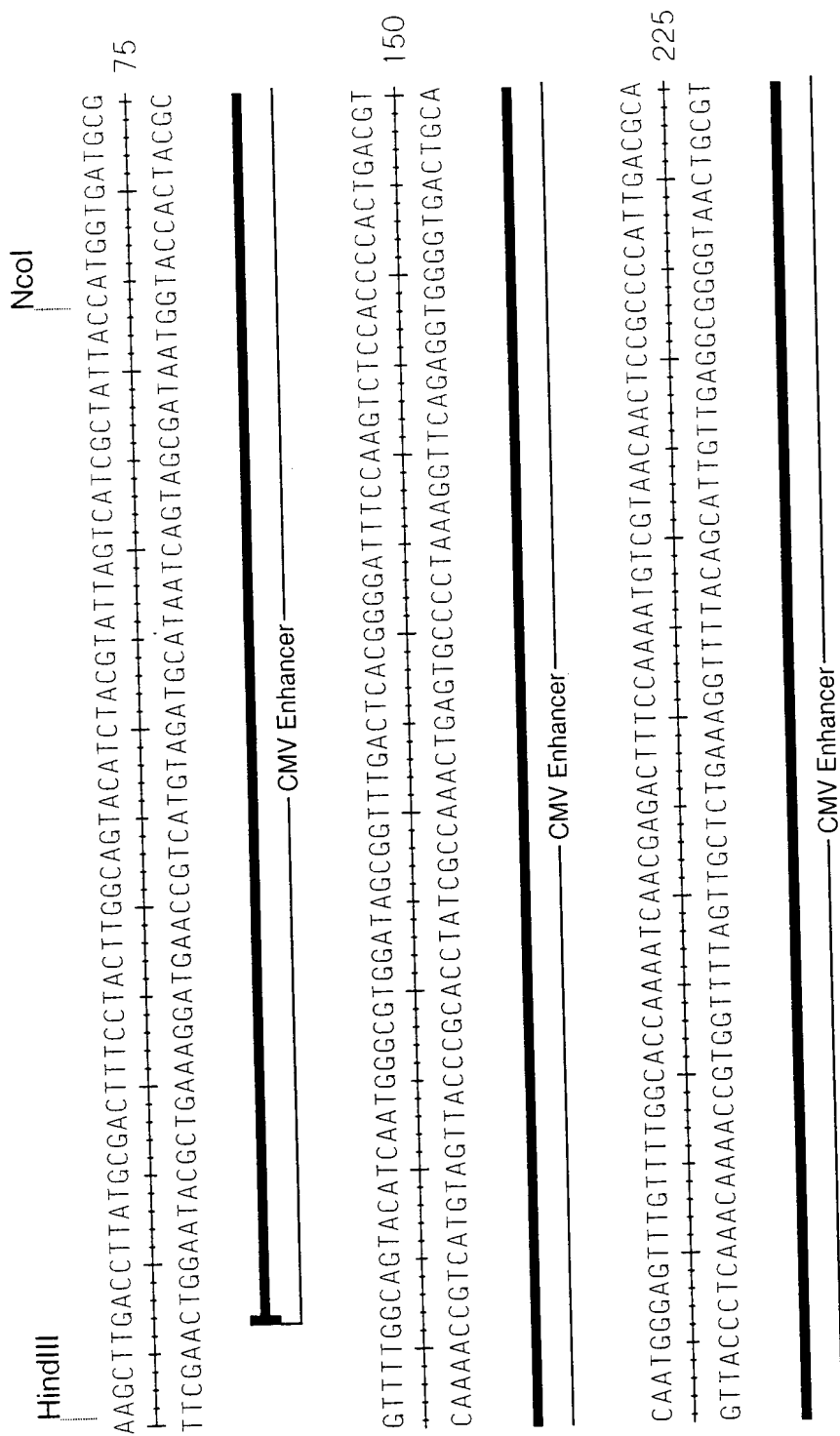


FIG.31A

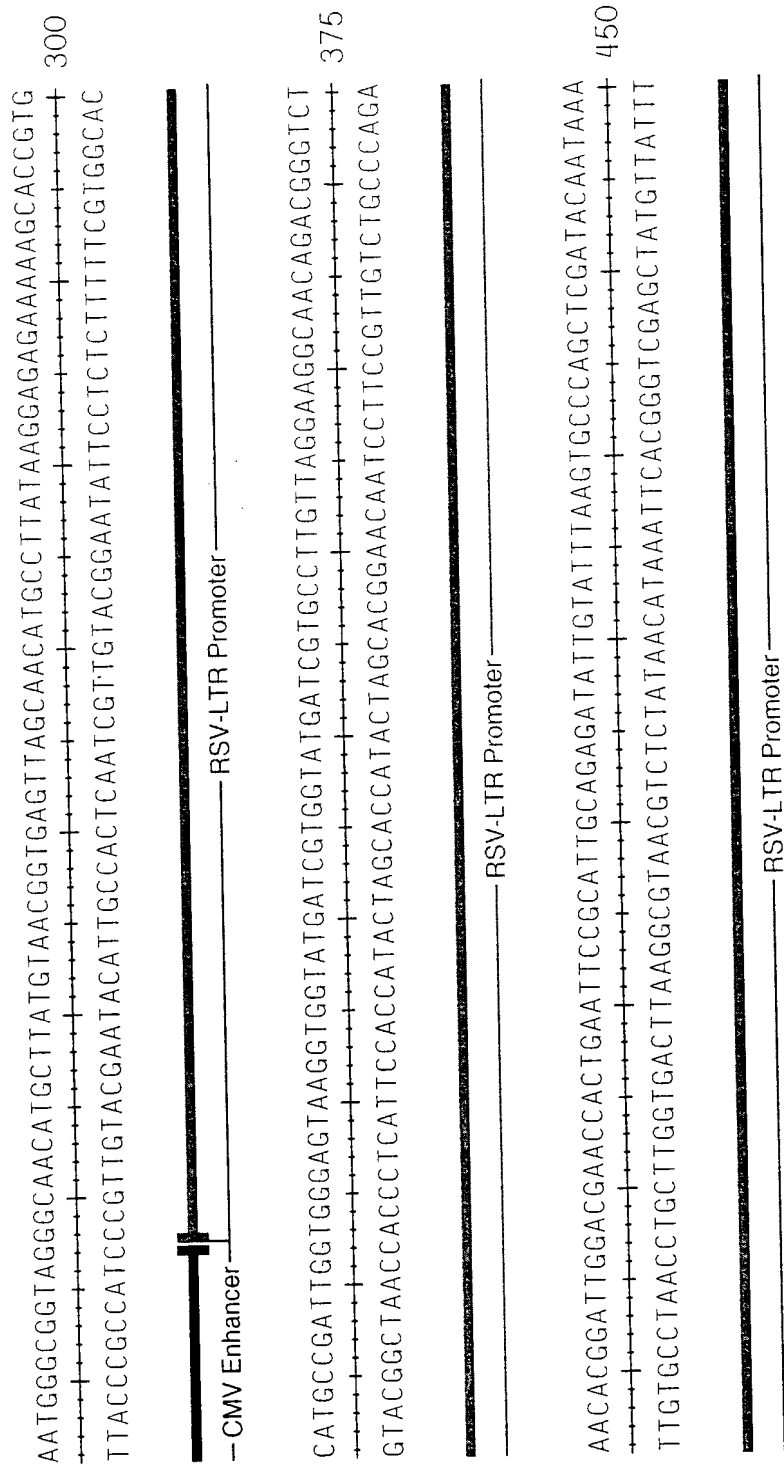


FIG.31B

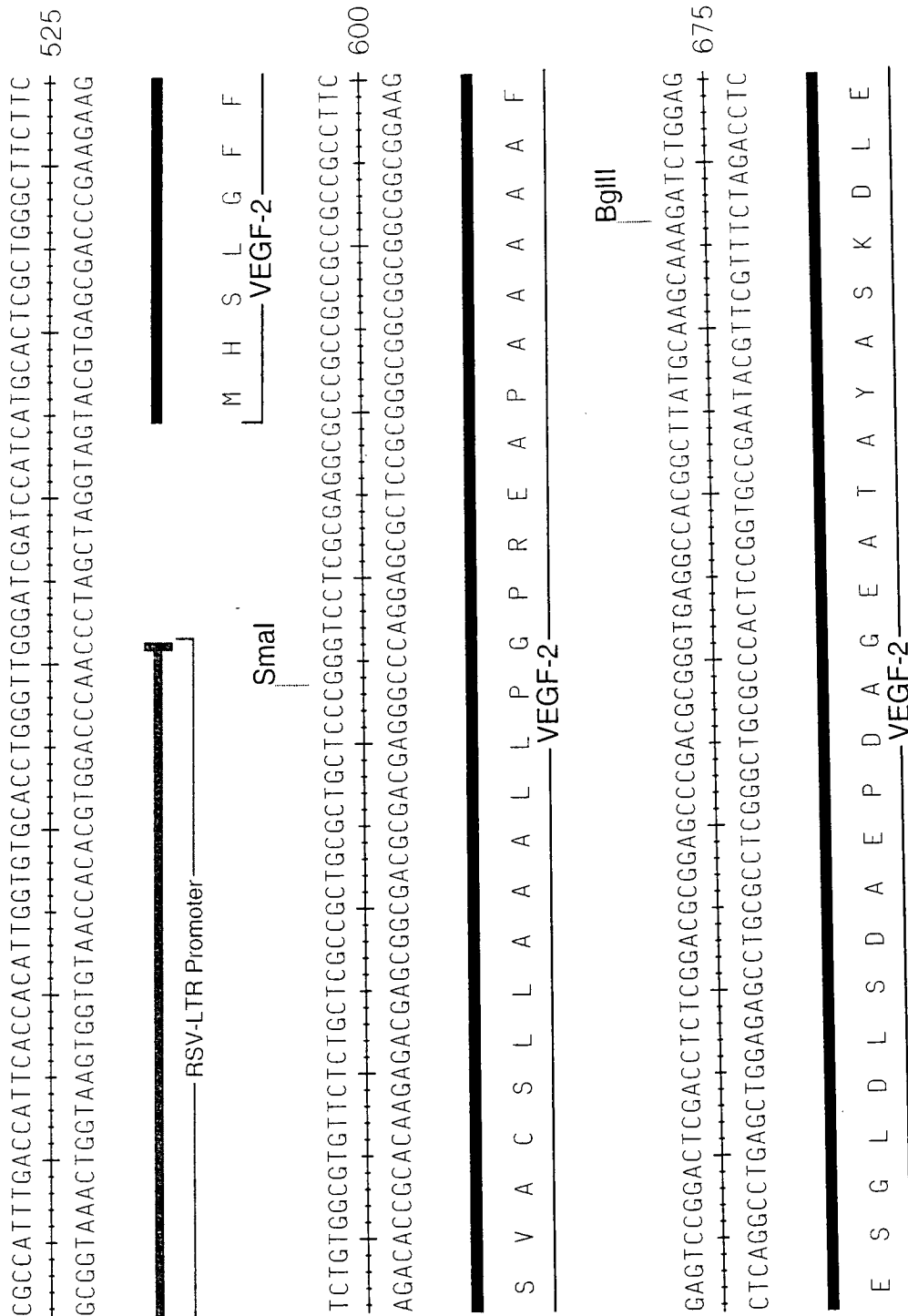


FIG.31C

GAGCAGTTACGGTCTGTGCCAGTGTAGATGAACATCATGACTGTACTCTACCCAGAATAATTGGAAAAATGTACAAG 750  
CTCGTCAATGCCAGACACAGGTCACATCTACTTGAGTACTGACATGAGATGGGTCTTTATAACCTTTTACATGTTT  
E Q L R S V S S V D E L M T V L Y P E Y W K M Y K  
VEGF-2

TGTCAGCTAAGGAAAGGAGGCTGGCAACATAACAGAGAACAGGCCAACCTCAACTCAAGGACAGAAAGAGACTATA 825  
ACAGTCGATTCCCTTCCCTCCGACCGTTGTATIGTCTCTTGTCGGTGGAGTTGAGTTCCCTGCTTCTCIGATAT  
C O L R K G G W O H N R E Q A N L N S R T E E T I  
VEGF-2

PstII BglII  
AAATTGCTGCAGCACATTATAATACAGAGATCTTGAAAAGTATTGATAAATGAGTGGAGAAAGACATCAATGCAATG 900  
TTTAAACGACGTCGTGTAATATTATGTCCTAGAACCTTTTCATAACTATTACTCACCTCTTTCTGAGTTACGTAC  
K F A A A H Y N T E I L K S I D N E W R K T Q C M  
VEGF-2

FIG.31D

CCACGGGAGGIGTGATAGATGTGGGAAGGAGTTTGGAGTCGGGACAAACACCTTCTTTAAACCTCCAIGTIG 975  
GGTGCCCTCCACACATATCTACACCCCTTCCCTCAAACCTCAGCGCTGTTTGTGGAAGAAATTTGGAGGTACACAC  
P R E V C I D V G K E F G V A T N T F F K P P C V  
VEGF-2

PstI  
TCCGTCTACAGATGTGGGGTIGCTGCAATAGTGAGGGGCTGCAGTGCAATGAACACCAGCAGCTACCTCAGC 1050  
AGGCAGATGCTACACCCCCAACGACGTTATCACTCCCCGACGTCACGTACTTGTGTCGTGCTCGATGGAGTCG  
S V Y R C G C C N S E G L Q C M N T S T S Y L S  
VEGF-2

AAGACGTTATTTGAAATTACAGTGCCCTCTCTCTCAAGGCCCCAAACCAGTAACAATCAGTTTTTGCCAAATCACACT 1125  
TTCTGCAATAAACTTTAATGTCACGGGAGAGAGATTCCGGGGTTTGGTCATTGTTAGTCAAAACGGTTAGTGTGA  
K T L F E I T V P L S Q G P K P V T I S F A N H T  
VEGF-2

FIG.31E

1200  
TCCTGCCGATGCTAAGTGGATGTTACAGACAAGTTCCATTATTAGACGTTCCCTGCCAGCAACA  
AGGACGGCTACGTACAGATTGACCTACAAATGCTCTGTTCAAGTAAGGTAATAATCTGCAAGGACGGTCTGTGT  
S C R C M S K L D V Y R Q V H S I I R R S L P A T  
VEGF-2

PstI

1275  
CTACCACAGTGTACGGCAGCGAACAAGACCTGCCCCACCAATTACATGTGGAATAATCACAATCTGCAGATGCCCTG  
GATGGTGTACAGTCCGTGCTTCTCGACGGGGTGGTTAATGTACACCTTATTAGTGTAGACGCTCTACGGAC  
L P Q C Q A A N K T C P T N Y M W N N H I C R C L  
VEGF-2

1350  
GCTCAGGAAGATTTTATGTTTTCCTCGGATGCTGGAGATGACTCAACAGATGGATTCCATGACATCTGTGGACCA  
CGAGTCCTTCTAAAAATACAAAAGGAGCCCTACGACCTCTACTGAGTTGCTCTACCTAAGGTACTGTAGACACCTGGT  
A Q E D F M F S S D A G D D S T D G F H D I C G P  
VEGF-2

FIG.31F

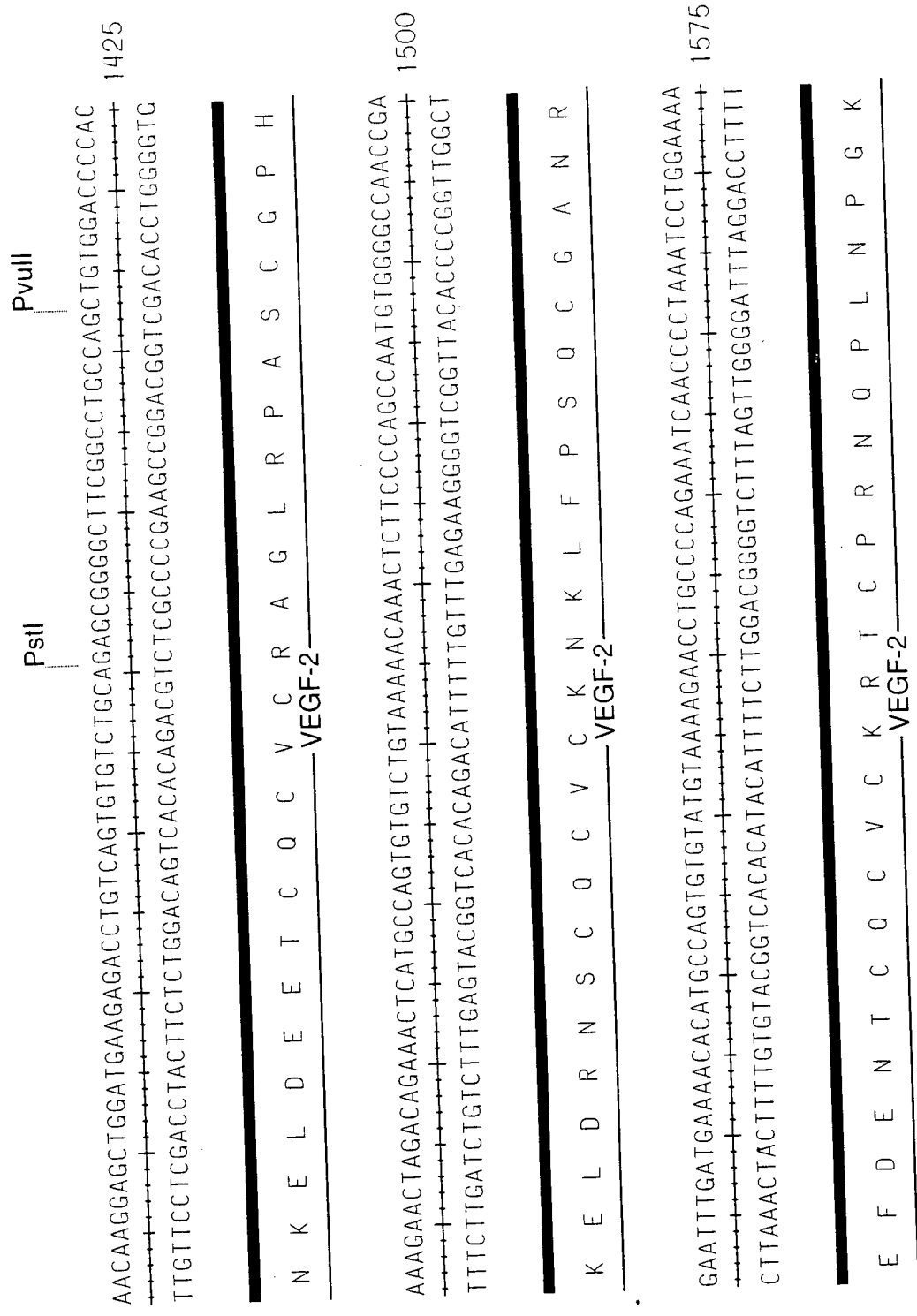


FIG.31G

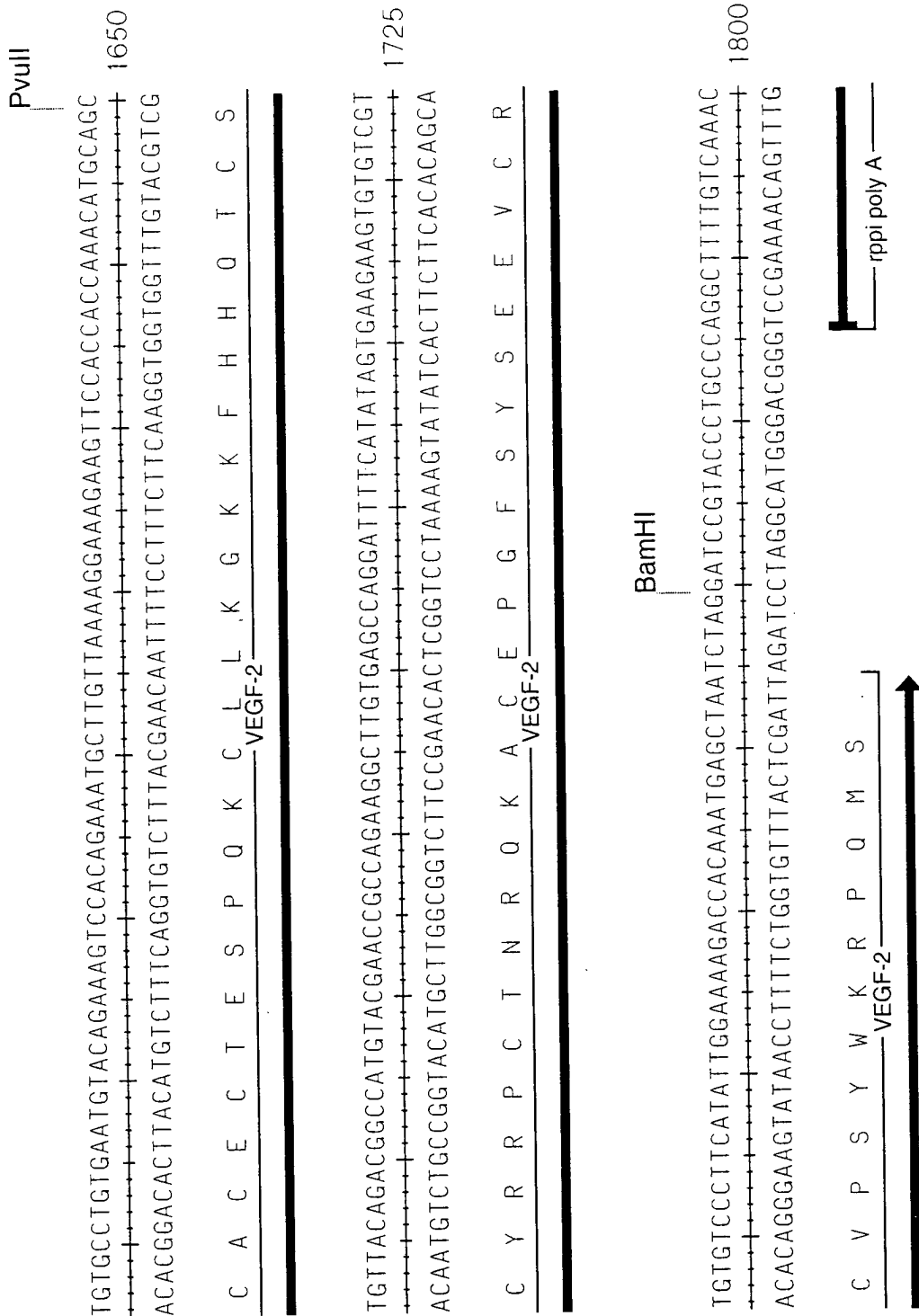
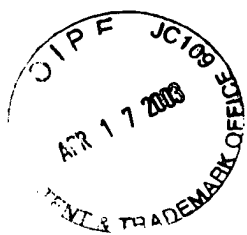


FIG.31H



1875  
AGCACCTTTGTGGTTCTCAGCTCTCTACCTGGTGTGGGGAGCGTGGATTCTTCTACACACCCA  
TCGTGGAACACCAAGAGTGAACCACTTCGAGAGATGGACCACACACCCCTCGCACCTAAGAAGATGTGTGGGT  
-----  
----- rppi poly A -----  
1950  
TGTCCCGCCGGAAGTGGAGGACCCACAAGGTAAGCTCTGCTCCTGAATTCTATCCCAAGTGCTAACTACCTGT  
ACAGGGCGGCGCTTCACCTCCTGGGTGTTCCATTTCGAGACGAGGACTTAAGATAGGGTTCACGATTGATGGGACA  
-----  
----- rppi poly A -----  
2025  
TTGTCTTTCACCCCTTGAGACCTTGTAATTTGTGCCCCCTAGGTGTGGAGGGTCTCAGGCTAACCAGTGGGGGGCACA  
AACAGAAAGTGGGAACCTCTGGAACATTTAACACGGGATCCACACCTCCACAGAGTCCGATTGGTCACCCCCCGTGT  
-----  
----- rppi poly A -----

FIG.31I

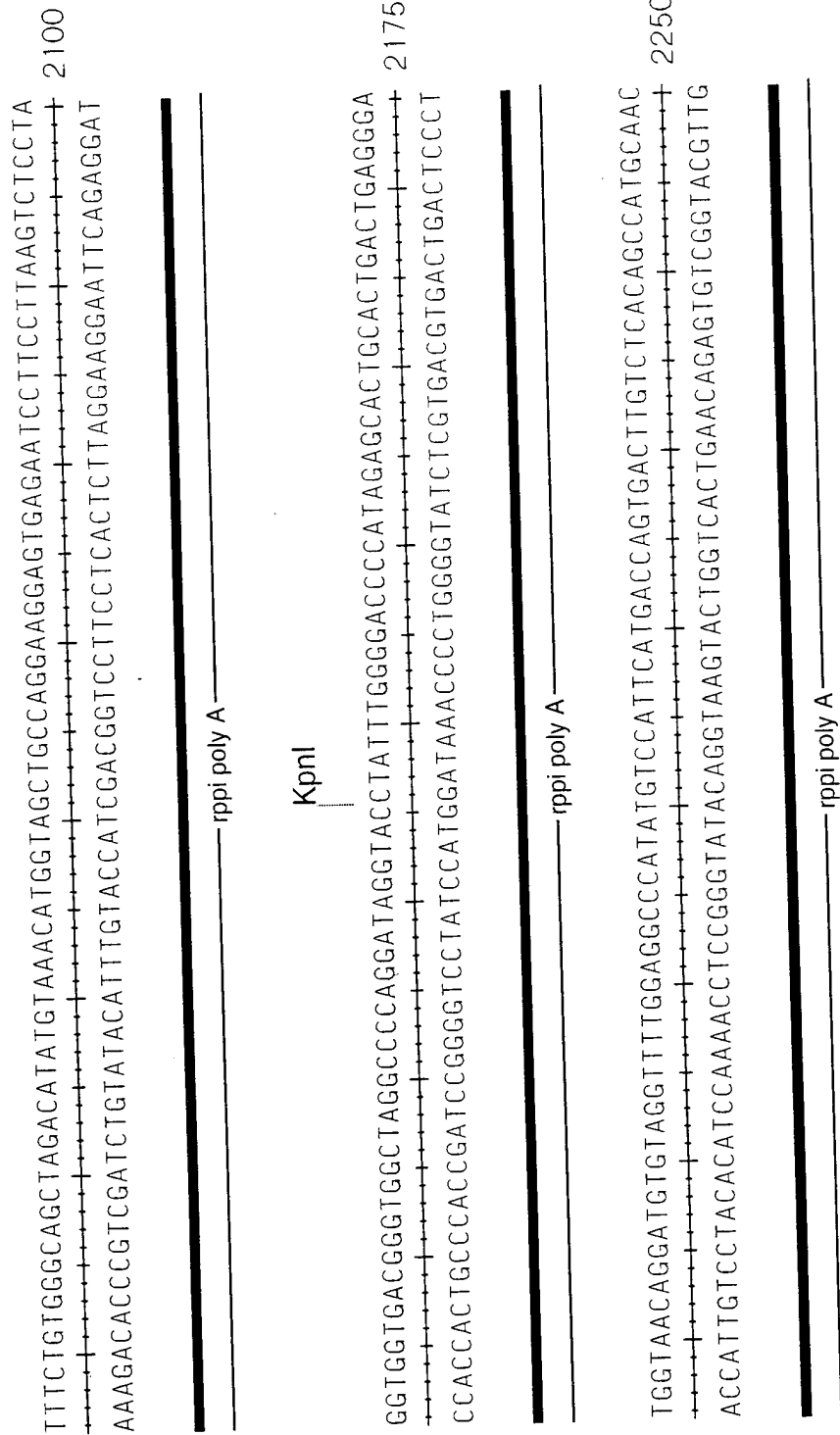


FIG.31J

2325  
CCTTGCCCTCCTGTGCTGACTTAGCAGGGGATAAAGTGAGAGAAAGCCTGGGCTAATCAGGGGGTCGCTCAGCTCC  
GGAACGGAGGACACGACTGAATCGTCCCCTATTTCACCTCTCTTTCGGACCCGATTAGTCCCCCAGCGAGTCGAGG

----- rppi poly A -----

2400  
TCCTAACTGGATTGTCCCTAATGCTCTTTGCTTCTGTGCTGATGCTCTGCCCCGTGCTGACATGACCTCCCTG  
AGGATTGACCTAACAGGATACACAGAAACGAAGACACGACCTACGAGACGGGACACGACTGTACTGGAGGGAC

----- rppi poly A -----

Smal

2475  
GCAGTGGCACAAC TGGAGCTGGGTGGAGGCCCGGGCAGGTGACCTTCAGACCTTGGCACTGGAGGTGGCCCCG  
CGTCACCGTGTGACCTCGACCCACCTCCGGGGCCCCCGTCCACTGGAAGTCTGGAACCGTGACCTCCACCCGGGCC

----- rppi poly A -----

2550  
CAGAAAGCGGGCATCGTGGATCAGTGTGCACCCAGCATCTGCTCTCTCTACCAACTGGAGAAGTACTGCAACTAG  
GTCTTCGGCGCGTAGCACCTAGTCACGACGTGGTCGTAGACGAGAGAGATGGTTGACCTCTTGATGACGTTGATC

----- rppi poly A -----

FIG.31K

2625  
GCCCACTACCTGTCCACCCCTCTGCAATGAATAAAACCTTTGAAAGAGCACTACAAGTTGTGTACATGC  
CGGGTGGTGAATGGGACAGGTGGGGAGACGTTACTTATTTTGGAACTTTCTCGTGATGTTCAACACACATGTACG

----- rppi poly A -----

2700  
GTGCATGTGCATATGTGGTGGGGGGAACATGAGTGGGGCTGGCTGGAGTGGTCGGGCTTAATCTATCTGGCA  
CAGTACACGTATACACACGCCCCCTTGTACTCACCCTGACCGACCTCACCAGCGCGAATTAGATAGACCGT

----- rppi poly A -----

PvuII XbaI

2775  
GCTGTCTAGACGTAATCATGGTCATAGCTGTTTCCCTGTGTGAAATTTATCCGCTCACAATCCACACAACATA  
CGACAGATCTGCATTAGTACCAGTATCGACAAAGGACACACTTTAACAAATAGCGGAGTGTAAAGGTGTGTAT

2850  
CGAGCCGGAAGCATAAAGGTAAAGCCCTGGGGTGCCCTAATGAGTGAGCTAACTCACATTAAATTCGCTTGGCTCA  
GCTCGGCCTTCGTATTTACATTTTCGGACCCACGGATTACTCACTCGATTGAGTGTAAATTAACGCAACGCGAGT

FIG.31L

PvuII

CTGCCCCGCTTTCAGTCGGGAACCTGTCGTGCCAGCTGCATTAAATGAATCGGCCAACGGCGGGGAGAGGCGGT 2925  
GACGGCGGAAGGTCAGCCCCTTTGGACAGCACGGTCGACGTAATTACTTAGCCGGTTGCGGCGCCCTCTCCGCCA  
TTGCGTATTGGGCGCTCTTCGGCTTCCTCGCTCACTGACTCGCTCGCTCGGTTCGTTTCGGCTGCGGGCGAGCGGT 3000  
AACGCATAACCCGCGAGAAGGCGAAGGAGCGAGTGACTGAGCGACGCGAGCCAGCAAGCCGACGCGCTCGCCAT  
TCAGCTCACTCAAAGGCGGTAAATACGGTTATCCACAGAAATCAGGGGATAACGCAGGAAAGAACATGTGAGCAAAA 3075  
AGTCGAGTGAGTTCCGCCATTATGCCCAATAGGTGTCCTTAGTCCCTATTGCGTCCCTTCTTGACACTCGTTTT  
GGCCAGCAAAAGGCCAGGAACCGTAAAAAGGCCGCTGCTGGCGTTTTTCCATAGGCTCCGCCCCCTGACGAG 3150  
CCGTCGTTTTCCGGTCCCTGGCATTTTTCCGGGCAACGACCGCAAAAAGGTATCCGAGGCGGGGGGACTGCTC

FIG.31M



CATCAGGCTCAAGTCAGAGGTGGCGAAACCCGACAGGACTATAAGATACCGGCGTTTCCCCCT 3225  
GTAGTTTTTAGCTGCGAGTTCAGTCTCCACCGCTTGGGCTGTCCGATAATTTCTATGGTCCGCAAGGGGA  
GGAAGCTCCCTCGTGGCTCTCCTGTTCGACCCCTGCCGCTTACCGGATACCTGTCCGCTTTCTCCCTTCGGGA 3300  
CCTTCGAGGAGCACCGGAGAGGACAAGCTGGGACGGCGAATGGCCTATGGACAGGCGGAAAGAGGAGGCCCT  
AGCGTGGCGCTTCTCATAGCTCACGCTGTAGGTATCTCAGTTCGGTGTAGGTCTCGTCCGCTCCAAGCTGGGCTGT 3375  
TCGCACCGCGAAAGAGTATCGAGTGGGACATCCATAGAGTCAAGCCACATCCAGCAAGCGAGGTTCGACCCGACA  
GTGCACGAAACCCCGTTCAGCCCGACCGCTGCGCCTTATCCGGTAACTATCGTCTTGAGTCCAACCCGGTAAGA 3450  
CACGTGCTTGGGGGCAAGTCGGCTGGCGACGGGAA TAGGCCATTGATAGCAGAACTCAGGTGGGCCATTCT  
CAGGACTTATCGCCACTGGCAGCAGCCACTGGTAACAGGATTAGCAGAGCGAGGTATGTAGGCGGTGCTACAGAG 3525  
GTGCTGAATAGCGGTGACCGTCTCGTGGTGACCATTGTCTAATCGTCTCGCTCCATACATCCGCCACGATGCTC

FIG.31N

TTCTTGAAGTGGTGGCCTAACTACGGCTACACTAGAAGAACAGTATTTGGTATCTGCGCTCTGCTGAAGCCAGTT 3600  
AAGAACTTCACCACCGGATTGATGCCGATGTGATCTTCTTGTCATAAACCATAGACGCGGAGACGACTTCGGTCAA  
ACCTTCGGAAAAAGAGTTGGTAGCTCTTGATCCGGCAAAACAAACCACCGCTGGTAGCGGTGGTTTTTTTGTTC  
TGGAGCCTTTTTCTCAACCATCGAGAACTAGGCCGTTTGTGGTGGCGACCATCGCCACCAAAAAACAAACG 3675  
AAGCAGCAGATTACGGCGAGAAAAAGGATCTCAAGAAGATCCTTTTGATCTTTTCTACGGGGTCTGACGCTCAG 3750  
TTCGTCGTCCTAATGCCGGTCTTTTTTCTAGAGTCTCTAGGAACTAGAAAAGATGCCCCAGACTGCGGAGTC  
Sall  
TGGAACGAAACACGTTAAGGGATTTTGGTCATGAGATTATCGTCGACCAAAAGCGGCCATCGTGCCTCCCCAC 3825  
ACCTTGCTTTTGAGTGCAATTCCCTAAACCACTACTCTAATAGCAGCTGGTTTCGCCGGTAGCACGGAGGGGTG

FIG.310

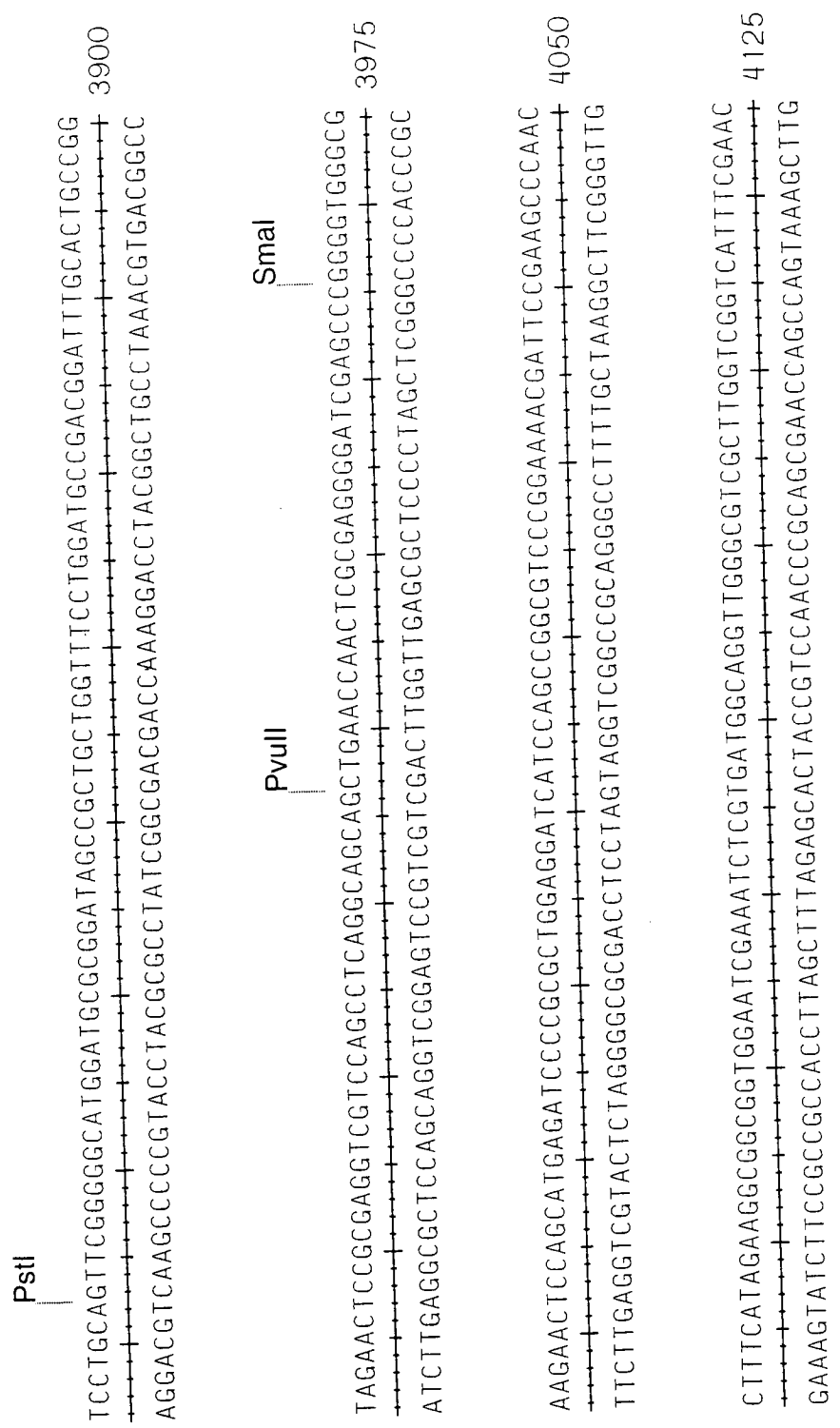


FIG.31P



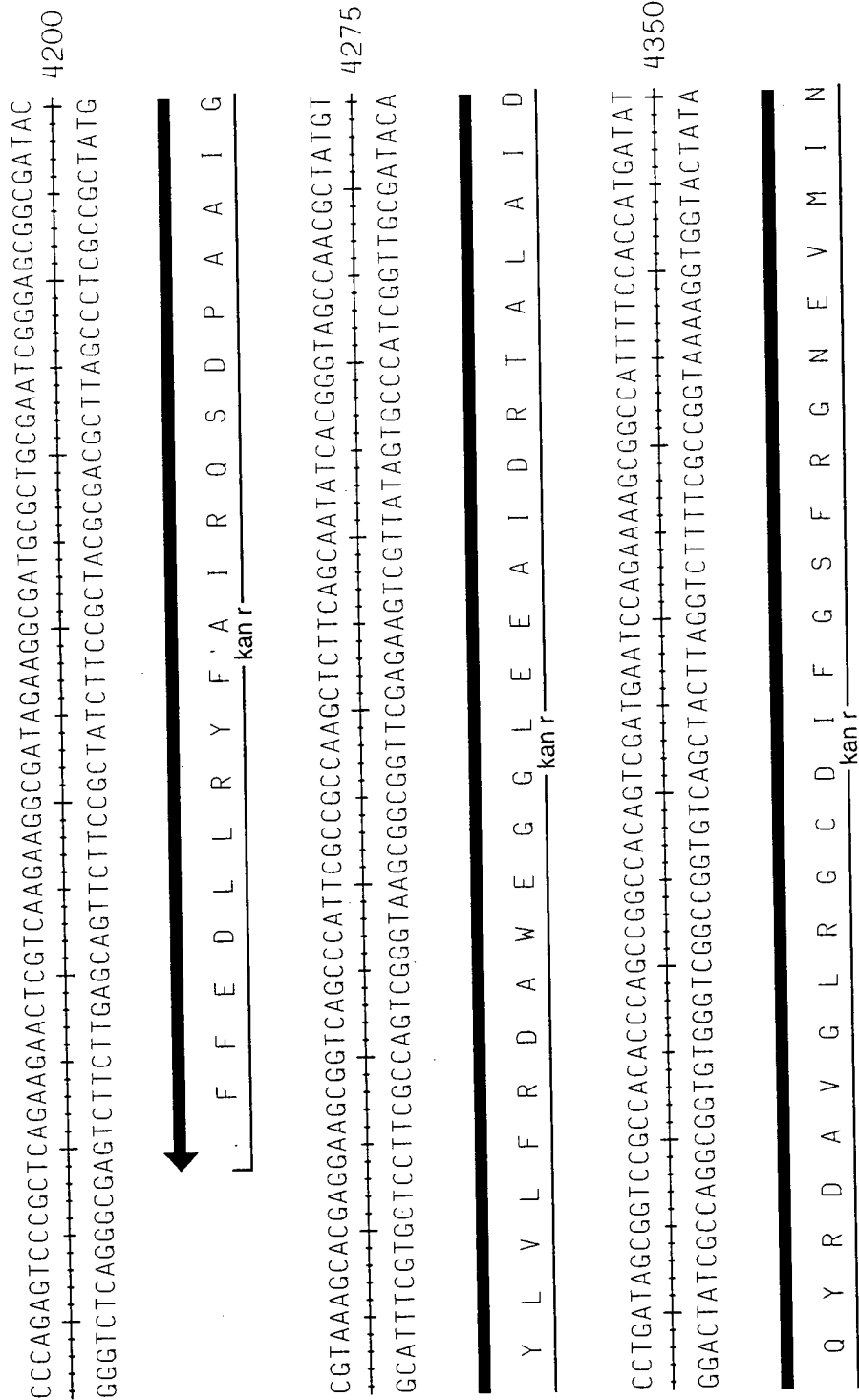


FIG.31Q

NcoI

TCGGCAAGCAGGCATCGCCATGGGTCACGACGAGATCCTCGCCGTCGGGCATGCGCGCCTTGAGCCTGGCGAACA  
 4425  
 AGCCGTTGTCGTCGTCAGCGGTACCCAGTGTCTCTAGGAGCGGCAGCCCCGTACGCGCGGAACCTCGGACCGCTTGT

P L C A D G H T V V L D E G D P M R A K L R A F L  
 kan r

GTTCGGCTGGCGGAGCCCCCTGATGCTCTTCGTCCAGATCATCTGATCGACAAGACCGGCTTCCATCCGAGTAC  
 4500  
 CAAGCCGACCGGCTCGGGGACTACGAGAAGCAGGCTAGTAGGACTAGCTGTCTGCGCGAAGGTAGGCTCATG

E A P A L G Q H E E D L D D Q D V L G A E M R T R  
 kan r

GTGCTCGCTCGATGCGATGTTTCGCTTGGTTCGAATGGGCAGGTAGCCGGATCAAGCGTATGCAGCCGCCGCA  
 4575  
 CACGAGCGAGCTACGCTACAAAGCGAACCACCAGCTTACCCGTCCATCGGCCCTAGTTCGCATACGTCGGCGGCGGT

A R E I R H K A O H D F P C T A P D L T H L R R M  
 kan r

FIG.31R

TTGCATCAGCCATGATGATACTTTCTCGGCAGGAGCAAGGTGAGATGACAGGAGATCCTGCCCCCGGCACTTCGC 4650  
AACGTAGTCGGTACTACCTATGAAAGAGCCGTCCTCGTTCCTACTCTAGGACGGGGCGGTGAAGCG  
A D A M I S V K E A P A L H S S L L D Q G P V E G  
PvuII  
CCAATAGCAGCCAGTCCCTTCCCGCTTCAGTGACAACGTCGAGCACAGCTGCGCAAGGAACGCCCGTCGTGGCCA 4725  
GGTTATCGTCGGTCAGGGAAGGGCGAAGTCACCTGTGAGCTCGTGTGACGCGTTCCTTGCGGGCAGCACCCGGT  
L L L W D R G A E T V V D L V A A C P V G T T A L

FIG.31S

PstI

GCCACGATAGCCGGCTGCCTCGTCTGCAGTTCAATCAGGGCACGGACAGGTCGGTCTTGACAAAAAGAACCG  
 4800  
 CGGTGCTATCGGCGGACGGAGCAGGACGTCAAGTAAGTCCCCTGGCTGTCCAGCCAGAACGTTTTCTTGGC

W S L R A A E D Q L E N L A G S L D T K V F L V P  
 kan r

GCGCCCCCTGCGCTGACAGCCGGAACACGGCGGCATCAGAGCAGCCGATTGTCTGTTGTGCCCAGTCATAGCCGA  
 4875  
 CCGCGGGACGCGACTGTGCGCCCTTGTCGCCCGGTAGTCTCGCTAACAGACAACACGGGTGAGTATCGGCT

R G Q A S L R F V A A D S C G I T O O A W D Y G F  
 kan r

ATAGCCTCTCCACCAAGCGGCGGAGAACCTGCGTGCAATCCAATCTGTTCAATCATGCGAAACGATCCATC  
 4950  
 TATCGGAGAGGTGGTTCGCCGGCTCTTGGACGCACGTTAGGTAGAACAAGTTAGTACGCTTGTCTAGGAGTAG

L R E V W A A P S G A H L G D O E I M  
 kan r

FIG.31T

BglII

CTGTCTCTTGATCAGATCTTGATCCCCCTGCGCCATCAGATCCTTGGCGGCAAGCAATCCAGTTTACITTGC  
5025  
GACAGAGAACTAGTCTAGAACTAGGGGACGGGTAGTCTAGGAACCGCCGTTCTTTCCGGTAGGTCAAAATGAAACG

PvuII

AGGGCTTCCCAACCTTACCAGAGGGGCGCCCAAGCTGGCAATTCGGGTTTCGCTTGCTGTCCATAAAACCGCCAGT  
5100  
TCCCGAAGGGTTGGAAATGGTCTCCCGCGGGGTCGACCGTTAAGGCCAAGCGAACGACAGGTATTTTGGCGGGTCA

CTAGCTATCGCCATGTAGCCCACTGCAAGCTACCTGCTTCTCTTTGCGCTTTCGCTTTCCTTGTCCAGATAG  
5175  
GATCGATAGCGGTACATTCGGGTGACGTTTCGATGGACGAAAGAGAAACGCGAACGCAAAAGGGAACAGGTCTATC

CCCAGTAGCTGACATTCATCCGGGGTCAGCACCGTTTCTGCGGACGGCTTTCACGIGTTCGCTTCCCTTTAGC  
5250  
GGGTATCGACTGTAAAGTAGGCCCCCAGTCGTGGCAAGACGCTGACCCGAAAGATGCACAAGGCGAAGGAAATCG

AGCCCTTGGCCCTGAGTGTCTTGGCGCAGCGTG  
5283  
TCGGGAACGCGGGACTCACGAACGCGCTCGCAC

FIG.31U